GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 5, 2004, 15:41:05 ; Search time 18 Seconds
(without alignments)
1310.432 Million cell updates/sec

Title: US-09-846-512-2
Perfect score: 2443
Sequence: 1 MGENDPPAVEAPFSFRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2432.5	99.6	454	1	TMS3_HUMAN	P57727 homo sapien
2	2226	91.1	453	1	TMS3_MOUSE	Q8k1t0 mus musculu
3	882	36.1	492	1	TMS2_HUMAN	O15393 homo sapien
4	875	35.8	490	1	TMS2_MOUSE	Q9jiq8 mus musculu
5	695.5	28.5	455	1	TMS5_MOUSE	Q9er04 mus musculu
6	689.5	28.2	457	1	TMS5_HUMAN	Q9h3s3 homo sapien
7	677	27.7	435	1	TMS4_MOUSE	Q8vca5 mus musculu
8	674	27.6	417	1	HEPS_HUMAN	P05981 homo sapien
9	669.5	27.4	1035	1	ENTK_BOVIN	P98072 bos taurus
10	664.5	27.2	1019	1	ENTK_HUMAN	P98073 homo sapien
11	663.5	27.2	1034	1	ENTK_PIG	P98074 sus scrofa
12	659.5	27.0	436	1	HEPS_MOUSE	O35453 mus musculu
13	658	26.9	437	1	TMS4_HUMAN	Q9nrs4 homo sapien
14	654.5	26.8	416	1	HEPS_RAT	Q05511 rattus norv
15	651	26.6	1069	1	ENTK_MOUSE	P97435 mus musculu
16	579.5	23.7	638	1	KAL_RAT	P14272 rattus norv
17	578.5	23.7	811	1	TMS6_MOUSE	Q9dbi0 mus musculu
18	571	23.4	418	1	HATT_HUMAN	O60235 homo sapien
19	570.5	23.4	638	1	KAL_MOUSE	P26262 mus musculu
20	560	22.9	811	1	TMS6_HUMAN	Q8iu80 homo sapien
21	549.5	22.5	638	1	KAL_HUMAN	P03952 homo sapien
22	543.5	22.2	855	1	ST14_HUMAN	Q9y5y6 homo sapien
23	532.5	21.8	324	1	TEST_MOUSE	Q9jhj7 mus musculu
24	527	21.6	761	1	NETR_MOUSE	O08762 mus musculu
25	526	21.5	338	1	PLMN_HORSE	P80010 equus cabal
26	523.5	21.4	790	1	PLMN_PIG	P06867 sus scrofa
27	523	21.4	855	1	ST14_MOUSE	P56677 mus musculu
28	522.5	21.4	422	1	DES1_HUMAN	Q9ul52 homo sapien
29	520.5	21.3	1042	1	CORI_HUMAN	Q9y5q5 homo sapien
30	511.5	20.9	311	1	TRYG_MOUSE	Q9qul7 mus musculu
31	507	20.8	314	1	TEST_HUMAN	Q9y6m0 homo sapien
32	506.5	20.7	1113	1	CORI_MOUSE	Q9z319 mus musculu
33	505	20.7	875	1	NETR_HUMAN	P56730 homo sapien
34	504	20.6	273	1	MCT7_MOUSE	Q02844 mus musculu
35	504	20.6	625	1	FA11_HUMAN	P03951 homo sapien
36	502	20.5	275	1	TRYT_CANFA	P15944 canis famil
37	502	20.5	810	1	PLMN_HUMAN	P00747 homo sapien
38	502	20.5	812	1	PLMN_MOUSE	P20918 mus musculu
39	500.5	20.5	343	1	PLMN_SHEEP	P81286 ovis aries
40	499	20.4	273	1	TRYT_SHEEP	Q9xsm2 ovis aries
41	499	20.4	810	1	PLMN_ERIEU	Q29485 erinaceus e
42	495.5	20.3	437	1	ACRO_RAT	P29293 rattus norv
43	495	20.3	270	1	TRYT_MERUN	P50342 meriones un
44	495	20.3	810	1	PLMN_MACMU	P12545 macaca mula
45	495	20.3	812	1	PLMN_BOVIN	P06868 bos taurus

ALIGNMENTS

RESULT 1
TMS3_HUMAN
ID TMS3_HUMAN STANDARD; PRT; 454 AA.
AC P57727;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Transmembrane protease, serine 3 (EC 3.4.21.-) (Serine protease
DE TADG-12) (Tumor associated differentially-expressed gene-12 protein).
GN TMPRSS3 OR TADG12 OR ECHOS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND T).
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=20521358; PubMed=11068177;
RA Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N.,
RA Wang Y., Parmley T.H., O'Brien T.J.;
RT "Ovarian tumor cells express a novel multi-domain cell surface serine
RT protease.";
RL Biochim. Biophys. Acta 1502:337-350(2000). ✓ NOV 15, 2000
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND D), AND VARIANT ILE-53.
RX MEDLINE=20578749; PubMed=11137999;
RA Scott H.S., Kudoh J., Wattenhofer M., Shibuya K., Berry A., Chrast R.,
RA Guipponi M., Wang J., Kawasaki K., Asakawa S., Minoshima S.,
RA Younus F., Mehdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C.,
RA Rossier C., Korostishevsky M., Gal A., Shimizu N., Bonne-Tamir B.,
RA Antonarakis S.E.;
RT "Insertion of beta-satellite repeats identifies a transmembrane
RT protease causing both congenital and childhood onset autosomal
RT recessive deafness.";
RL Nat. Genet. 27:59-63(2001).
RN [3]
RP SUBCELLULAR LOCATION, AND FUNCTION IN ENAC CLEAVAGE.
RX MEDLINE=22281255; PubMed=12393794;
RA Guipponi M., Vuagniaux G., Wattenhofer M., Shibuya K., Vazquez M.,
RA Dougherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M.,
RA Buchet K., Reymond A., Hummler E., Marzella P.L., Kudoh J.,
RA Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.;
RT "The transmembrane serine protease (TMPRSS3) mutated in deafness
RT DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro.";
RL Hum. Mol. Genet. 11:2829-2836(2002).
RN [4]
RP VARIANTS DFBN8/DFNB10 CYS-251 AND LEU-404.
RX MEDLINE=21354482; PubMed=11462234;
RA Masmoudi S., Antonarakis S.E., Schwede T., Ghorbel A.M., Gratri M.,
RA Pappasavas M.P., Drira M., Elgaied-Boulila A., Wattenhofer M.,
RA Rossier C., Scott H.S., Ayadi H., Guipponi M.;
RT "Novel missense mutations of TMPRSS3 in two consanguineous Tunisian
RT families with non-syndromic autosomal recessive deafness.";
RL Hum. Mutat. 18:101-108(2001).
RN [5]
RP VARIANTS DFBN8/DFNB10 TRP-109; PHE-194 AND ARG-407, AND VARIANTS

```
RP   ILE-53; SER-111 AND VAL-253.
RX   MEDLINE=21317610; PubMed=11424922;
RA   Ben-Yosef T., Wattenhofer M., Riazuddin S., Ahmed Z.M., Scott H.S.,
RA   Kudoh J., Shibuya K., Antonarakis S.E., Bonne-Tamir B.,
RA   Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A.,
RA   Nance W.E., Wilcox E.R., Friedman T.B., Morell R.J.;
RT   "Novel mutations of TMPRSS3 in four DFNB8/B10 families segregating
RT   congenital autosomal recessive deafness.";
RL   J. Med. Genet. 38:396-400(2001).
RN   [6]
RP   VARIANT DFBN8/DFNB10 GLY-103, AND VARIANTS ASN-173 AND THR-426.
RX   MEDLINE=21904597; PubMed=11907649;
RA   Wattenhofer M., Di Iorio V., Rabionet R., Dougherty L., Pampanos A.,
RA   Schwede T., Montserrat-Sentis B., Arbones L., Iliades T.,
RA   Pasquadibisceglie A., D'Amelio M., Alwan S., Rossier C., Dahl H.-H.M.,
RA   Petersen M.B., Estivill X., Gasparini P., Scott H.S.,
RA   Antonarakis S.E.;
RT   "Mutations in the TMPRSS3 gene are a rare cause of childhood
RT   nonsyndromic deafness in Caucasian patients.";
RL   J. Mol. Med. 80:124-131(2002).
CC   -!- FUNCTION: Probable protease. Seems to be capable of activating
CC       ENaC.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
CC       reticulum.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P57727-1; Sequence=Displayed;
CC       Name=B; Synonyms=C;
CC         IsoId=P57727-2; Sequence=VSP_005391;
CC       Name=D;
CC         IsoId=P57727-3; Sequence=VSP_005392;
CC       Name=T; Synonyms=Truncated, TADG-12V;
CC         IsoId=P57727-4; Sequence=VSP_005393, VSP_005394;
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues including fetal
CC       cochlea. Isoform T is found at increased levels in some
CC       carcinomas.
CC   -!- PTM: Undergoes autoproteolytic activation.
CC   -!- DISEASE: Defects in TMPRSS3 are a cause of childhood-onset
CC       autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072].
CC   -!- DISEASE: Defects in TMPRSS3 are a cause of congenital autosomal
CC       recessive neurosensory deafness 10 (DFNB10) [MIM:605316].
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF201380; AAG37012.1; -.
DR   EMBL; AB038157; BAB20077.1; -.
DR   EMBL; AB038158; BAB20078.1; -.
DR   EMBL; AB038159; BAB20079.1; -.
DR   EMBL; AB038160; BAB20080.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.079; -.
DR   Genew; HGNC:11877; TMPRSS3.
DR   MIM; 605511; -.
DR   MIM; 601072; -.
DR   MIM; 605316; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen;
KW   Endoplasmic reticulum; Deafness; Alternative splicing;
KW   Disease mutation; Polymorphism.
FT   DOMAIN        1     48       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     49     69       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                 (POTENTIAL).
FT   DOMAIN       70    454       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       72    108       LDL-RECEPTOR CLASS A.
FT   DOMAIN      109    205       SRCR.
FT   DOMAIN      217    454       SERINE PROTEASE.
FT   ACT_SITE    257    257       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    304    304       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    401    401       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE        216    217       CLEAVAGE (POTENTIAL).
FT   DISULFID     73     85       BY SIMILARITY.
FT   DISULFID     79     98       BY SIMILARITY.
FT   DISULFID     92    107       BY SIMILARITY.
FT   DISULFID    129    194       BY SIMILARITY.
FT   DISULFID    142    204       BY SIMILARITY.
FT   DISULFID    207    324       BY SIMILARITY.
FT   DISULFID    242    258       BY SIMILARITY.
FT   DISULFID    338    407       BY SIMILARITY.
FT   DISULFID    370    386       BY SIMILARITY.
FT   DISULFID    397    425       BY SIMILARITY.
FT   CARBOHYD    221    221       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1    127       Missing (in isoform B).
FT                                 /FTId=VSP_005391.
FT   VARSPLIC    318    454       EMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLN
FT                                 HAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG
FT                                 DSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSF
FT                                 LDWIHEQMERDLKT -> GTSGSLCGSAALPLFQEDLQLLI
FT                                 EAFL (in isoform D).
FT                                 /FTId=VSP_005392.
FT   VARSPLIC    261    293       DLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYH -> EIVA
FT                                 PRERADRRGRKLLCWRKPTKMKGPRPSHS (in isoform
FT                                 T).
FT                                 /FTId=VSP_005393.
FT   VARSPLIC    294    454       Missing (in isoform T).
FT                                 /FTId=VSP_005394.
FT   VARIANT      53     53       V -> I.
FT                                 /FTId=VAR_010781.
FT   VARIANT     103    103       D -> G (in DFNB8/DFNB10).
FT                                 /FTId=VAR_013490.
FT   VARIANT     109    109       R -> W (in DFNB8/DFNB10).
FT                                 /FTId=VAR_013491.
FT   VARIANT     111    111       G -> S.
FT                                 /FTId=VAR_013492.
FT   VARIANT     173    173       D -> N.
FT                                 /FTId=VAR_013493.
FT   VARIANT     194    194       C -> F (in DFNB8/DFNB10).
FT                                 /FTId=VAR_013494.
FT   VARIANT     251    251       W -> C (in DFNB8/DFNB10).
FT                                 /FTId=VAR_011678.
FT   VARIANT     253    253       I -> V (in dbSNP:2839500).
FT                                 /FTId=VAR_013101.
FT   VARIANT     404    404       P -> L (in DFNB8/DFNB10).
FT                                 /FTId=VAR_011679.
FT   VARIANT     407    407       C -> R (in DFNB8/DFNB10).
FT                                 /FTId=VAR_013495.
FT   VARIANT     426    426       A -> T.
```

```
  Query Match           99.6%;  Score 2432.5;  DB 1;  Length 454;
  Best Local Similarity  99.8%;  Pred. No. 2.7e-198;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG-GDASPVLNHA 359
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHA 360

Qy        360 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 420

Qy        420 FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              ||||||||||||||||||||||||||||||||||
Db        421 FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 454
```

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RESULT 2
TMS3_MOUSE
ID   TMS3_MOUSE     STANDARD;      PRT;   453 AA.
AC   Q8K1T0; Q8VDE0;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Transmembrane protease, serine 3 (EC 3.4.21.-).
GN   TMPRSS3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND FUNCTION IN ENAC
RP   CLEAVAGE.
RX   MEDLINE=22281255; PubMed=12393794;
RA   Guipponi M., Vuagniaux G., Wattenhofer M., Shibuya K., Vazquez M.,
RA   Dougherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M.,
RA   Buchet K., Reymond A., Hummler E., Marzella P.L., Kudoh J.,
RA   Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.;
RT   "The transmembrane serine protease (TMPRSS3) mutated in deafness
RT   DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro.";
RL   Hum. Mol. Genet. 11:2829-2836(2002).
CC   -!- FUNCTION: Probable protease. Seems to be capable of activating
CC       ENaC.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
CC       reticulum.
CC   -!- TISSUE SPECIFICITY: Expressed in the spiral ganglion, the cells
CC       supporting the organ of Corti and the stria vascularis.
CC   -!- PTM: Undergoes autoproteolytic activation.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ429216; CAD22137.1; -.
DR   EMBL; AJ300738; CAC83350.1; -.
DR   HSSP; P00761; 1AN1.
DR   MGD; MGI:2155445; Tmprss3.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen;
KW   Endoplasmic reticulum.
FT   DOMAIN        1     48       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     49     69       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       70    453       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       72    108       LDL-RECEPTOR CLASS A.
FT   DOMAIN      104    205       SRCR.
FT   DOMAIN      217    448       SERINE PROTEASE.
FT   ACT_SITE    257    257       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    304    304       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    400    400       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE        216    217       CLEAVAGE (POTENTIAL).
FT   DISULFID     73     85       BY SIMILARITY.
FT   DISULFID     79     98       BY SIMILARITY.
FT   DISULFID     92    107       BY SIMILARITY.
FT   DISULFID    129    194       BY SIMILARITY.
FT   DISULFID    142    204       BY SIMILARITY.
FT   DISULFID    207    324       BY SIMILARITY.
FT   DISULFID    242    258       BY SIMILARITY.
FT   DISULFID    338    406       BY SIMILARITY.
FT   DISULFID    369    385       BY SIMILARITY.
FT   DISULFID    396    424       BY SIMILARITY.
FT   CARBOHYD    221    221       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    117    117       L -> H (IN REF. 1; CAC83350).
FT   CONFLICT    246    246       V -> I (IN REF. 1; CAC83350).
SQ   SEQUENCE   453 AA;  49491 MW;  1ABCBF10AF6E1EF6 CRC64;
```

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  Query Match           91.1%;  Score 2226;  DB 1;  Length 453;
  Best Local Similarity  89.2%;  Pred. No. 8.1e-181;
  Matches  404;  Conservative   24;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              |||||||| ||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 MGENDPPAAEAPFSFRSLFGLDDLKISPVAPDGDAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              |||||||||||||||||| |||||||| |||||||||: ||||||||| || | ||||
Db         61 LALAIGLGIHFDCSGKYRCHSSFKCIELTARCDGVSDCKNAEDEYRCVRVSGQRAALQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              |||:|:|||||||| ||| :|||||||||||||:||| :|| ||: :||||:||| |||
Db        121 TAAAWRTMCSDDWKSHYAKIACAQLGFPSYVSSDHLRVDALEEQFQGDFVSINHLLSDDK 180
```

```
Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||:|||| |||||||:|:||| | ||| |||||||| |:||||| ||||||||
Db        181 VTALHHSVYMREGCTSGHVVTLKCSACGTRTGYSPRIVGGNMSSLTQWPWQVSLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              |||||||||||:|||||||||| |||||:|||||||:|:| ||||||||:|||||||||
Db        241 LCGGSVITPLWIVTAAHCVYDLYHPKSWTVQVGLVSLMDSPVPSHLVEKIIYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              |||||||||: |||||:| |||:||||||||||||:||||||||||||||||||||||||
Db        301 LGNDIALMKLSEPLTFDETIQPICLPNSEENFPDGKLCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLKGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||||:||||||||||:||||||
Db        421 GIGCAEVNKPGVYTRITSFLDWIHEQLERDLKT 453
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RESULT 3
TMS2_HUMAN
ID TMS2_HUMAN STANDARD; PRT; 492 AA.
AC O15393; Q9BXX1;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 2 precursor (EC 3.4.21.-).
GN TMPRSS2 OR PRSS10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97468144; PubMed=9325052;
RA Paoloni-Giacobino A., Chen H., Peitsch M.C., Rossier C.,
RA Antonarakis S.E.;
RT "Cloning of the TMPRSS2 gene, which encodes a novel serine protease
RT with transmembrane, LDLRA, and SRCR domains and maps to 21q22.3.";
RL Genomics 44:309-320(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309069; PubMed=11414763;
RA Teng D.H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.;
RT "Mutation analyses of 268 candidate genes in human tumor cell lines.";
RL Genomics 74:352-364(2001).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RX MEDLINE=21139112; PubMed=11245484;
RA Afar D.E.H., Vivanco I., Hubert R.S., Kuo J., Chen E., Saffran D.C.,
RA Raitano A.B., Jakobovits A.;
RT "Catalytic cleavage of the androgen-regulated TMPRSS2 protease results
RT in its secretion by prostate and prostate cancer epithelia.";
RL Cancer Res. 61:1686-1692(2001).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=21104370; PubMed=11169526;
RA Vaarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihko P.T.;
RT "Expression of transmembrane serine protease TMPRSS2 in mouse and
RT human tissues.";
RL J. Pathol. 193:134-140(2001).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Activated by
CC cleavage and secreted.
CC -!- TISSUE SPECIFICITY: Expressed strongly in small intestine. Also
CC expressed in prostate, colon, stomach and salivary gland.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U75329; AAC51784.1; -.
DR EMBL; AF123453; AAD37117.1; -.
DR EMBL; AF270487; AAK29280.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.247; -.
DR Genew; HGNC:11876; TMPRSS2.
DR MIM; 602060; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50068; LDLRA_2; 1.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen;
KW Polymorphism.

FT	CHAIN	1	255	TRANSMEMBRANE PROTEASE, SERINE 2, NON-CATALYTIC CHAIN.
FT	CHAIN	256	492	TRANSMEMBRANE PROTEASE, SERINE 2, CATALYTIC CHAIN.
FT	DOMAIN	1	84	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	85	105	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	106	492	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	112	149	LDL-RECEPTOR CLASS A.
FT	DOMAIN	150	242	SRCR.
FT	DOMAIN	256	492	SERINE PROTEASE.
FT	ACT_SITE	296	296	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	345	345	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	441	441	CHARGE RELAY SYSTEM.
FT	SITE	255	256	CLEAVAGE (POTENTIAL).
FT	DISULFID	113	126	BY SIMILARITY.
FT	DISULFID	120	139	BY SIMILARITY.
FT	DISULFID	133	148	BY SIMILARITY.
FT	DISULFID	172	231	BY SIMILARITY.
FT	DISULFID	185	241	BY SIMILARITY.
FT	DISULFID	244	365	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	281	297	BY SIMILARITY.
FT	DISULFID	410	426	BY SIMILARITY.
FT	DISULFID	437	465	BY SIMILARITY.
FT	CARBOHYD	213	213	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	449	449	K -> N (in dbSNP:1056602).
FT				/FTId=VAR_011692.
FT	MUTAGEN	255	255	R->Q: LOSS OF CLEAVAGE.
FT	MUTAGEN	441	441	S->A: LOSS OF ACTIVITY.
FT	CONFLICT	160	160	M -> V (IN REF. 3).
FT	CONFLICT	242	242	I -> L (IN REF. 1).
FT	CONFLICT	329	329	E -> Q (IN REF. 1).
FT	CONFLICT	489	491	RAD -> KAN (IN REF. 1).

SQ SEQUENCE 492 AA; 53891 MW; CAB44FD174A9076B CRC64;

Query Match 36.1%; Score 882; DB 1; Length 492;
Best Local Similarity 45.7%; Pred. No. 5.2e-67;
Matches 188; Conservative 54; Mismatches 149; Indels 20; Gaps 10;

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Qy          52 IVIGIIALILALAIGLGIHF---DCSGK-YRCRSSFKCIELIARCDGVSDCKDGEDEYRC 107
               : :|   :  ||| ||   |    ||     | ||  ||     |||| | |||| ||
Db          89 LTLGTFLVGAALAAGLLWKFMGSKCSNSGIECDSSGTCINPSNWCDGVSHCPGGEDENRC 148

Qy         108 VRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ 164
               ||: | | :||:::   ||  :| |||  :|    ||  :|:  :: ||  :   |
Db         149 VRLYGPNFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKNNFYSSQGIVDDSGSTS 208

Qy         165 FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNM 222
               | :   |  ::   |    |:||    : |:|  ||:|:| |||      |  ||||||
Db         209 FMKLNTSAGNV---DIYKKLYHS----DACSSKAVVSLRCIACGVNLNSSRQSRIVGGES 261

Qy         223 SLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLD 279
               :|   |||| ||   |  |:||||:||| ||:|||||   |  |  ||   |::  | :
Db         262 ALPGAWPWQVSLHVQNVHVCGGSIITPEWIVTAAHCVEKPLNNPWHWTAFAGILRQSFMF 321

Qy         280 NPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCW 339
                 | : |||:: |  |  |   ||||||||  |||||:::||||||        ::||
Db         322 YGA-GYQVEKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCW 380

Qy         340 TSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGD 399
               |||||||: |  | ||| | | ||  : || | ||  :|:|:|:|||:| | |||||||
Db         381 ISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGD 440

Qy         400 SGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD 450
               ||||||  :  :| |:| ||:| |||:  :|||  |  | |||: ||  |
Db         441 SGGPLVTSKNNIWWLIGDTSWGSGCAKAYRPGVYGNVMVFTDWIYRQMRAD 491
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RESULT 4
TMS2_MOUSE
ID TMS2_MOUSE STANDARD; PRT; 490 AA.
AC Q9JIQ8; Q9JKC4; Q9QY82;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Transmembrane protease, serine 2 (EC 3.4.21.-) (Epitheliasin) (Plasmic
DE transmembrane protein X).
GN TMPRSS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=BALB/c;
RX MEDLINE=21104370; PubMed=11169526;
RA Vaarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihko P.T.;
RT "Expression of transmembrane serine protease TMPRSS2 in mouse and
RT human tissues.";
RL J. Pathol. 193:134-140(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Han J., Kim S.;
RT "Putative transmembrane protease X.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20148617; PubMed=10683448;
RA Jacquinet E.J., Rao N.V., Rao G.V., Hoidal J.R.;
RT "Cloning, genomic organization, chromosomal assignment and expression
RT of a novel mosaic serine proteinase: epitheliasin.";
RL FEBS Lett. 468:93-100(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Activated by
CC cleavage and secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed mainly in prostate and kidney.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC --

CC --
DR EMBL; AF199362; AAF97867.1; -.
DR EMBL; AF243500; AAF64186.1; -.
DR EMBL; AF113596; AAF21308.1; -.
DR EMBL; BC038393; AAH38393.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.247; -.
DR MGD; MGI:1354381; Tmprss2.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00530; SRCR; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50068; LDLRA_2; 1.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen.
FT CHAIN 1 253 TRANSMEMBRANE PROTEASE, SERINE 2, NON-
FT CATALYTIC CHAIN.
FT CHAIN 254 490 TRANSMEMBRANE PROTEASE, SERINE 2,
FT CATALYTIC CHAIN.
FT DOMAIN 1 83 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 84 104 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 105 490 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 111 149 LDL-RECEPTOR CLASS A.
FT DOMAIN 150 242 SRCR.
FT DOMAIN 254 490 SERINE PROTEASE.
FT ACT_SITE 294 294 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 343 343 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 439 439 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE 253 254 CLEAVAGE (POTENTIAL).

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FT   DISULFID     76    125       BY SIMILARITY.
FT   DISULFID    119    138       BY SIMILARITY.
FT   DISULFID    132    147       BY SIMILARITY.
FT   DISULFID    171    230       BY SIMILARITY.
FT   DISULFID    184    240       BY SIMILARITY.
FT   DISULFID    243    363       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    279    295       BY SIMILARITY.
FT   DISULFID    408    424       BY SIMILARITY.
FT   DISULFID    435    463       BY SIMILARITY.
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    212    212       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    474    474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    122    122       S -> L (IN REF. 3).
FT   CONFLICT    178    178       S -> N (IN REF. 3).
FT   CONFLICT    320    320       Y -> H (IN REF. 1).
FT   CONFLICT    474    474       N -> D (IN REF. 1).
SQ   SEQUENCE   490 AA;  53479 MW;  07D2B03EA4D8A1A9 CRC64;

  Query Match             35.8%;  Score 875;  DB 1;  Length 490;
  Best Local Similarity   41.0%;  Pred. No. 2e-66;
  Matches  193;  Conservative   66;  Mismatches  146;  Indels   66;  Gaps   13;

Qy         28 PVAPDADAVAAQILSLLPLKFFPIIV-----------IGII----------------A 58
              ||||:          :| | :::|  |                :|              :
Db         31 PVAPNG-------YNLYPAQYYPSPVPQYAPRITTQASTSVIHTHPKSSGAPCTSKSKKS 83

Qy         59 LILALAIGLGI--------------HFDCS-GKYRCRSSFKCIELIARCDGVSDCKDGED 103
              | ||||:|  :                :||  :  | ||  ||     ||||: | :|||
Db         84 LCLALALGTVLTGAAVAAVLLWRFWDSNCSTSEMECGSSGTCISSSLWCDGVAHCPNGED 143

Qy        104 EYRCVRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSS 160
              | ||||:-||: :|||:::   :|  :| |||    |   ||  :|:  :: ||  :   |
Db        144 ENRCVRLYGQSFILQVYSSQRKAWYPVCQDDWSESYGRAACKDMGYKNNFYSSQGIPDQS 203

Qy        161 LEGQPREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRR-GYSSRIVG 219
                 | :  ||  ::   |    |:||   : |:|  ||:|:|  || |     |||||
Db        204 GATSFMKLNVSSGNV---DLYKKLYHS----DSCSSRMVVSLRCIECGVRSVKRQSRIVG 256

Qy        220 GNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYD-LYLPKSWTIQVGLV--S 276
              |  :    |||| ||  || |:|||:||| ||:|||||| : |  |: ||  |::  |
Db        257 GLNASPGDWPWQVSLHVQGVHVCGGSIITPEWIVTAAHCVEEPLSGPRYWTAFAGILRQS 316

Qy        277 LLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336
              |:      | |||:: |  |  |   ||||||||  || ||::::||||||      :
Db        317 LMFY-GSRHQVEKVISHPNYDSKTKNNDIALMKLQTPLAFNDLVKPVCLPNPGMMLDLDQ 375

Qy        337 VCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSC 396
               || |||||| :  |  | ||| | ||||     || : :|  :|:|:|:|||:| | ||||
Db        376 ECWISGWGATYEKGKTSDVLNAAMVPLIEPSKCNSKYIYNNLITPAMICAGFLQGSVDSC 435

Qy        397 QGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM 447
              |||||||||  :  :| |:| ||:| |||:  :||||  || | |||::||
Db        436 QGDSGGPLVTLKNGIWWLIGDTSWGSGCAKALRPGVYGNVTVFTDWIYQQM 486


RESULT 5
TMS5_MOUSE
ID   TMS5_MOUSE     STANDARD;      PRT;   455 AA.
AC   Q9ER04; Q9ER02; Q9ER03;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN   TMPRSS5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC   TISSUE=Brain;
RA   Mitsui S., Yamaguchi N.;
RT   "cDNA cloning of mouse spinesin.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 4).
RC   TISSUE=Brain;
RA   Mitsui S., Yamaguchi N.;
RT   "Molecular cloning of mouse type 4 spinesin.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=4;
CC         IsoId=Q9ER04-1; Sequence=Displayed;
CC       Name=1;
CC         IsoId=Q9ER04-2; Sequence=VSP_005397, VSP_005398;
CC       Name=2;
CC         IsoId=Q9ER04-3; Sequence=VSP_005395;
CC       Name=3;
CC         IsoId=Q9ER04-4; Sequence=VSP_005396;
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; AB016229; BAB20276.1; -.
DR   EMBL; AB016230; BAB20277.1; -.
DR   EMBL; AB016423; BAB20278.1; -.
DR   EMBL; AB041037; BAB40328.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.313; -.
DR   MGD; MGI:1933407; Tmprss5.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW   Glycoprotein; Alternative splicing.
FT   DOMAIN       1     49       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    50     70       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN      71    455       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN     112    207       SRCR.
FT   DOMAIN     218    455       SERINE PROTEASE.
FT   ACT_SITE   258    258       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   308    308       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   405    405       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE       217    218       CLEAVAGE (POTENTIAL).
FT   DISULFID   135    196       BY SIMILARITY.
FT   DISULFID   148    206       BY SIMILARITY.
FT   DISULFID   209    328       BY SIMILARITY.
FT   DISULFID   243    259       BY SIMILARITY.
FT   DISULFID   374    390       BY SIMILARITY.
FT   DISULFID   401    429       BY SIMILARITY.
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     1    144       Missing (in isoform 2).
FT                               /FTId=VSP_005395.
FT   VARSPLIC     1     10       Missing (in isoform 3).
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FT                                /FTId=VSP_005396.
FT   VARSPLIC      1    182       Missing (in isoform 1).
FT                                /FTId=VSP_005397.
FT   VARSPLIC    183    192       GGLVEEAWKP -> MEAQVGLLWV (in isoform 1).
FT                                /FTId=VSP_005398.
FT   CONFLICT    325    325       D -> G (IN REF. 1; BAB20277).
SQ   SEQUENCE   455 AA;  49632 MW;  5CFC31789C6899AA CRC64;

  Query Match             28.5%;  Score 695.5;  DB 1;  Length 455;
  Best Local Similarity   35.1%;  Pred. No. 2.9e-51;
  Matches  150;  Conservative   63;  Mismatches  161;  Indels   53;  Gaps   12;

Qy          52 IVIGIIALILALAIG---LGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYR-- 106
               :::|:: |:    |    | ::   :       : :  |:   | ||| |   |:|
Db          50 VILGVLGLLLAGAGIASWLLVLYLWPAASPSISGTLQEEEMTLNCPGVS-C---EEELLPS 105

Qy         107 -----CVRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVS 159
                   |: |:: :|||    |   |  :| : |         | ||          : :|
Db         106 LPKTVSFRINGEDLLLQVQVRARPDWLLVCHEGWSPALGMHICKSLGHIRLTQHKAVNLS 165

Qy         160 SLEGQFREEFVSIDHLLPDDKVTALHHSVYVREG------------CASGHVVTLQCTAC 207
                ::    :||  :                | |             | || :|:|:|: |
Db         166 DIKLNRSQEFAQLS----------------ARPGGLVEEAWKPSANCPSGRIVSLKCSEC 209

Qy         208 GHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK- 266
               |  |  :||||||      :||||||:      | || ||: | |::|||||:|   | :
Db         210 G-ARPLASRIVGGQAVASGRWPWQASVMLGSRHTCGASVLAPHWVVTAAHCMYSFRLSRL 268

Qy         267 -SWTIQVGLVSLLDNPAPSH---LVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQP 322
                || :  ||||         |   :||||: |  |  :    |:||::|  |: |:: :
Db         269 SSWRVHAGLVS--HGAVRQHQGTMVEKIIPHPLYSAQNHDYDVALLQLRTPINFSDTVDA 326

Qy         323 VCLPNSEENFPDGKVCWTSGWGATEDG-GDASPVLNHAAVPLISNKICNHRDVYGGIISP 381
               ||||  |: || |  || |||| |:     :|  |     |||:|  :||   :| | ::
Db         327 VCLPAKEQYFPWGSQCWVSGWGHTDPSHTHSSDTLQDTMVPLLSTHLCNSSCMYSGALTH 386

Qy         382 SMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLD 441
               ||||||| |  |:|||||||||||     | |||  |:| |||| |:|||| :|  |||
Db         387 RMLCAGYLDGRADACQGDSGGPLVCPSGDTWHLVGVVSWGRGCAEPNRPGVYAKVAEFLD 446

Qy         442 WIHEQME 448
               |||: ::
Db         447 WIHDTVQ 453


RESULT 6
TMS5_HUMAN
ID   TMS5_HUMAN     STANDARD;      PRT;   457 AA.
AC   Q9H3S3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN   TMPRSS5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11741986;
RA   Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;
RT   "Spinesin/TMPRSS5, a novel transmembrane serine protease, cloned from
RT   human spinal cord.";
RL   J. Biol. Chem. 277:6806-6812(2002).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in
CC       neurons, in their axons, and at the synapses of motoneurons in the
CC       spinal cord.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ----------------------------------------------------------------------

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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB028140; BAB20375.1; -.
DR   HSSP; P00763; 1DPO.
DR   Genew; HGNC:14908; TMPRSS5.
DR   MIM; 606751; -.
DR   MEROPS; S01.313; -.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; FALSE_NEG.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW   Glycoprotein.
FT   DOMAIN        1     49       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     50     70       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       71    457       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      112    207       SRCR.
FT   DOMAIN      218    457       SERINE PROTEASE.
FT   ACT_SITE    258    258       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    308    308       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    405    405       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE        217    218       CLEAVAGE (POTENTIAL).
FT   DISULFID    135    196       BY SIMILARITY.
FT   DISULFID    148    206       BY SIMILARITY.
FT   DISULFID    209    328       BY SIMILARITY.
FT   DISULFID    243    259       BY SIMILARITY.
FT   DISULFID    374    390       BY SIMILARITY.
FT   DISULFID    401    429       BY SIMILARITY.
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   457 AA;  49574 MW;  64406AB4985A2651 CRC64;

  Query Match             28.2%;  Score 689.5;  DB 1;  Length 457;
  Best Local Similarity   35.2%;  Pred. No. 9.4e-51;
  Matches  149;  Conservative   58;  Mismatches  175;  Indels   41;  Gaps    8;

Qy          53 VIGIIALILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGG 112
               |:| : |:    :|  :      | | :: : |              :| |    |
Db          51 VLGALGLLAGAGVGSWLLV----LYLCPAASQPIS--------GTLQDEEITLSCSEASA 98

Qy         113 QNAVL-------------------QVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVS 152
               : |:|                  ||     | :| : |             | ||
Db          99 EEALLPALPKTVSFRINSEDFLLEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHLRLTH 158

Qy         153 SDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRG 212
               : :: ::    :||  :     |     |  :    |  | || ||:|:|: ||  |
Db         159 HKGVNLTDIKLNSSQEFAQLSPRLGG----FLEEAWQPRNNCTSGQVVSLRCSECG-ARP 213

Qy         213 YSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK--SWTI 270
                :||||||      :||||||:      | |||||: | |::|||||::    | :  || :
Db         214 LASRIVGGQSVAPGRWPWQASVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRV 273

Qy         271 QVGLVS-LLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSE 329
                ||||    |   |||:|: | |  :    |:||::|    | |:: :  ||||  |
Db         274 HAGLVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALLRLQTALNFSDTVGAVCLPAKE 333
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Qy        330 ENFPDGKVCWTSGWGATEDGGD-ASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGY 388
              ::|| |  || |||| |      :| :|    ||| | ::||   || | ::| ||||||
Db        334 QHFPKGSRCWVSGWGHTHPSHTYSSDMLQDTVVPLFSTQLCNSSCVYSGALTPRMLCAGY 393

Qy        389 LTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              | |  |:||||||||||| :  |:|||  |:|  ||| | |||| :|  ||||||:  :
Db        394 LDGRADACQGDSGGPLVCPDGDTWRLVGVVSWGRACAEPNHPGVYAKVAEFLDWIHDTAQ 453

Qy        449 RDL 451
                |
Db        454 DSL 456


RESULT 7
TMS4_MOUSE
ID   TMS4_MOUSE     STANDARD;      PRT;   435 AA.
AC   Q8VCA5;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Transmembrane protease, serine 4 (EC 3.4.21.-) (Channel-activating
DE   protease 2) (mCAP2).
GN   TMPRSS4 OR CAP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22144321; PubMed=12149280;
RA   Vuagniaux G., Vallet V., Jaeger N.F., Hummler E., Rossier B.C.;
RT   "Synergistic activation of ENaC by three membrane-bound channel-
RT   activating serine proteases (mCAP1, mCAP2, and mCAP3) and serum- and
RT   glucocorticoid-regulated kinase (Sgk1) in Xenopus oocytes.";
RL   J. Gen. Physiol. 120:191-201(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Probable protease. Seems to be capable of activating
CC       ENaC.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AY043240; AAK85307.1; -.
DR   EMBL; BC021368; AAH21368.1; -.
DR   HSSP; P00761; 1AN1.
DR   MEROPS; S01.034; -.
DR   MGD; MGI:2384877; Tmprss4.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PROSITE; PS01209; LDLRA_1; FALSE_NEG.
DR   PROSITE; PS50068; LDLRA_2; FALSE_NEG.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor.
FT   DOMAIN       1     30       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     31    51       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN       52    435      EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       59    101      LDL-RECEPTOR CLASS A.
FT   DOMAIN       102   202      SRCR.
FT   DOMAIN       203   435      SERINE PROTEASE.
FT   ACT_SITE     243   243      CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE     288   288      CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE     385   385      CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE         202   203      CLEAVAGE (POTENTIAL).
FT   DISULFID     62    81       BY SIMILARITY.
FT   DISULFID     75    90       BY SIMILARITY.
FT   DISULFID     125   181      BY SIMILARITY.
FT   DISULFID     138   191      BY SIMILARITY.
FT   DISULFID     194   308      BY SIMILARITY.
FT   DISULFID     228   244      BY SIMILARITY.
FT   DISULFID     354   370      BY SIMILARITY.
FT   DISULFID     381   408      BY SIMILARITY.
FT   CARBOHYD     128   128      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     176   176      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  47495 MW;  DC52E45A43E01369 CRC64;

  Query Match           27.7%;  Score 677;  DB 1;  Length 435;
  Best Local Similarity  37.1%;  Pred. No. 1e-49;
  Matches  161;  Conservative   71;  Mismatches  154;  Indels   48;  Gaps   14;

Qy         45 PLKFFPIIVIGIIALILAL------AIGLGIHFDCSGKYR--CRSSFKCIELIARCDGVS 96
              | : |  : | |||::|:|      |: : :  |  ||   | |    |:    |||
Db         23 PQETFKKVGIPIIAVLLSLIALVIVALLIKVILD---KYYFICGSPLTFIQRGQLCDGHL 79

Qy         97 DCKDGEDEYRC----------VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYANVACA 143
              ||  |||| |           ||:    : ||| || :| ::| |::    |  ||
Db         80 DCASGEDEEHCVKDFPEKPGVAVRLSKDRSTLQVLDAATGTWASVCFDNFTEALAKTACR 139

Qy        144 QLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREG---CASGHVV 200
              |:|: |           :  ||   :  |  ||  :||     : |: |   | || :|
Db        140 QMGYDS-----------QPAFRAVEIRPDQNLPVAQVTGNSQELQVQNGSRSCLSGSLV 187

Qy        201 TLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVY 260
              :|:|  || :   : |:|||  : :  |||| |:|:   |:||||:: | ||:|||||
Db        188 SLRCLDCG-KSLKTPRVVGGVEAPVDSWPWQVSIQYNKQHVCGGSILDPHWILTAAHCFR 246

Qy        261 DLYLPKSWTIQVGLVSLLDNPAPSHLVEK--IVYHSKYKPKRLGNDIALMKLAGPLTFNE 318
                 || :: |  ::| | :||  | |  |   :   ||    ||||:|| ||||:
Db        247 KYLDVSSWKVRAG-SNILGN-SPSLPVAKIFIAEPNPLYPKE--KDIALVKLQMPLTFSG 302

Qy        319 MIQPVCLPNSEENFPDGKVCWTSGWGATED-GGDASPVLNHAAVPLISNKICNHRDVYGG 377
              ::|:||| |:|        |  ||| ||: ||  | :|  |:| :| :  ||  | | |
Db        303 SVRPICLPFSDEVLVPATPVWVIGWGFTEENGGKMSDMLLQASVQVIDSTRCNAEDAYEG 362
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Qy        378 IISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVT 437
              ::  |||||   || |:|||||||||:    : |::||  |:| ||   : |||||:||
Db        363 EVTAEMLCAGTPQGGKDTCQGDSGGPLMYHSDK-WQVVGIVSWGHGCGGPSTPGVYTKVT 421

Qy        438 SFLDWIHEQMERDL 451
              ::|:||:   : ::
Db        422 AYLNWIYNVRKSEM 435


RESULT 8
HEPS_HUMAN
ID   HEPS_HUMAN     STANDARD;      PRT;   417 AA.
AC   P05981;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine
DE   1).
GN   HPN OR TMPRSS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=88209431; PubMed=2835076;
RA   Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
RT   "A novel trypsin-like serine protease (hepsin) with a putative
RT   transmembrane domain expressed by human liver and hepatoma cells.";
RL   Biochemistry 27:1067-1074(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=91358502; PubMed=1885621;
RA   Tsuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S.,
RA   Chou S.H., Kurachi K.;
RT   "Hepsin, a cell membrane-associated protease. Characterization,
RT   tissue distribution, and gene localization.";
RL   J. Biol. Chem. 266:16948-16953(1991).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=93348237; PubMed=8346233;
RA   Torres-Rosado A., O'Shea K.S., Tsuji A., Chou S.H., Kurachi K.;
RT   "Hepsin, a putative cell-surface serine protease, is required for
RT   mammalian cell growth.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).
CC   -!- FUNCTION: Plays an essential role in cell growth and maintenance
CC       of cell morphology.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- TISSUE SPECIFICITY: Present in most tissues, with the highest
CC       level in liver.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M18930; AAA36013.1; -.
DR   EMBL; X07732; CAA30558.1; -.
DR   EMBL; X07002; CAA30058.1; -.
DR   EMBL; BC025716; AAH25716.1; -.
DR   PIR; S00845; S00845.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.224; -.
DR   Genew; HGNC:5155; HPN.
DR   MIM; 142440; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR   GO; GO:0008151; P:cell growth and/or maintenance; TAS.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor.
FT   CHAIN         1    162       SERINE PROTEASE HEPSIN, NON-CATALYTIC
FT                                CHAIN (POTENTIAL).
FT   CHAIN       163    417       SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
FT                                (POTENTIAL).
FT   DOMAIN        1     17       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     18     44       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       45    417       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      163    417       SERINE PROTEASE.
FT   ACT_SITE    203    203       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    257    257       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    353    353       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID    153    277       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    188    204       BY SIMILARITY.
FT   DISULFID    322    338       BY SIMILARITY.
FT   DISULFID    349    381       BY SIMILARITY.
FT   CARBOHYD    112    112       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   417 AA;  45011 MW;  B2086FF661E551D7 CRC64;

  Query Match             27.6%;  Score 674;  DB 1;  Length 417;
  Best Local Similarity   35.8%;  Pred. No. 1.7e-49;
  Matches  149;  Conservative   62;  Mismatches  143;  Indels   62;  Gaps   11;

Qy         59 LILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQ 118
              |:|  |||             :|:  : :: | |          ::    |:|   :| |
Db         26 LLLLTAIG-------------AASWAIVAVLLRSD--------QEPLYPVQVSSADARLM 64

Qy        119 VF--TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLL 176
              ||  |  :|: :||         | ::| ::||   ::    | |  :        :|
Db         65 VFDKTEGTWRLLCSSRSNARVAGLSCEEMGFLRALTHSELDVRTAGANGTSGFFCVDE-- 122

Qy        177 PDDKVTALHHSVYVRE-----GCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQ 231
                  | |:  : |       |  | :   |  || |:    |||||  : | :||||
Db        123 -----GRLPHTQRLLEVISVCDCPRGRFLAAICQDCGRRKLPVDRIVGGRDTSLGRWPWQ 177

Qy        232 ASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK------SWTIQVGLVSLLDNPAPSH 285
               ||:: | ||||||:::  |::|||||      |:       | :  | |:     :|
Db        178 VSLRYDGAHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRVFAGAVA---QASPHG 229
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Qy        286 L---VEKIVYHSKYKPKR------LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336
              |   |: :|||  | | |        |||||: |: ||   | |||||||  : :   |||
Db        230 LQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQALVDGK 289

Qy        337 VCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSC 396
              :|  :||| |:  |  : ||  | ||:||| :||  | ||  | | | ||||  ||:|:|
Db        290 ICTVTGWGNTQYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDAC 349

Qy        397 QGDSGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              |||||||  ||::       |:| |  |:| |||   |||||:|: | :|| : ::
Db        350 QGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWIFQAIK 405
```

RESULT 9
ENTK_BOVIN
ID ENTK_BOVIN STANDARD; PRT; 1035 AA.
AC P98072;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).
GN PRSS7 OR ENTK.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Duodenum;
RX MEDLINE=94329561; PubMed=8052624;
RA Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.;
RT "Enterokinase, the initiator of intestinal digestion, is a mosaic
RT protease composed of a distinctive assortment of domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
RN [2]
RP SEQUENCE OF 801-1035 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94043122; PubMed=8226855;
RA Lavallie E.R., Rehemtulla A., Racie L.A., Diblasio E.A.,
RA Ferenz C., Grant K.L., Light A., McCoy J.M.;
RT "Cloning and functional expression of a cDNA encoding the catalytic
RT subunit of bovine enterokinase.";
RL J. Biol. Chem. 268:23311-23317(1993).
RN [3]
RP SEQUENCE OF 801-827.
RC TISSUE=Intestine;
RX MEDLINE=92189715; PubMed=1799406;
RA Light A., Janska H.;
RT "The amino-terminal sequence of the catalytic subunit of bovine
RT enterokinase.";
RL J. Protein Chem. 10:475-480(1991).
CC -!- FUNCTION: Responsible for initiating activation of pancreatic
CC proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC A). It catalyzes the conversion of trypsinogen to trypsin which in
CC turn activates other proenzymes including chymotrypsinogen,
CC procarboxypeptidases, and proelastases.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC trypsinogen.
CC -!- SUBUNIT: Heterodimer of a catalytic (light) chain and a
CC multidomain (heavy) chain linked by a disulfide bond.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P98072-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P98072-2; Sequence=VSP_005386;
CC -!- TISSUE SPECIFICITY: Intestinal brush border.
CC -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -!- SIMILARITY: Contains 1 SRCR domain.
CC ---

CC ---
DR EMBL; U09859; AAB40026.1; -.
DR EMBL; L19663; AAA16035.1; -.
DR PIR; A43090; A43090.
DR PDB; 1EKB; 14-OCT-99.
DR MEROPS; S01.156; -.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000082; SEA_domain.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00057; ldl_recept_a; 2.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF01390; SEA; 1.
DR Pfam; PF00530; SRCR; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00192; LDLa; 2.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00200; SEA; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01209; LDLRA_1; 2.
DR PROSITE; PS50068; LDLRA_2; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
DR PROSITE; PS50024; SEA; 1.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;
KW Zymogen; Transmembrane; Repeat; Alternative splicing; 3D-structure;
KW Lipoprotein.

FT	CHAIN	1	800 NON-CATALYTIC CHAIN (HEAVY CHAIN).
FT	CHAIN	801	1035 CATALYTIC CHAIN (LIGHT CHAIN).
FT	DOMAIN	1	18 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	19	47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT			(POTENTIAL).
FT	DOMAIN	48	1035 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	54	169 SEA.
FT	DOMAIN	197	238 LDL-RECEPTOR CLASS A 1.
FT	DOMAIN	240	350 CUB 1.
FT	DOMAIN	358	520 MAM.
FT	DOMAIN	540	650 CUB 2.
FT	DOMAIN	657	695 LDL-RECEPTOR CLASS A 2.
FT	DOMAIN	694	787 SRCR.
FT	DOMAIN	801	1035 SERINE PROTEASE.
FT	ACT_SITE	841	841 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	892	892 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	987	987 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	LIPID	2	2 N-myristoyl glycine (Potential).
FT	DISULFID	199	212 BY SIMILARITY.

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FT   DISULFID    206    225       BY SIMILARITY.
FT   DISULFID    219    236       BY SIMILARITY.
FT   DISULFID    659    671       BY SIMILARITY.
FT   DISULFID    666    684       BY SIMILARITY.
FT   DISULFID    678    693       BY SIMILARITY.
FT   DISULFID    788    912       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    826    842       BY SIMILARITY.
FT   DISULFID    926    993       BY SIMILARITY.
FT   DISULFID    957    972       BY SIMILARITY.
FT   DISULFID    983   1011       BY SIMILARITY.
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    194    194       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    263    263       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    264    264       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    404    404       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    456    456       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    486    486       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    519    519       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    550    550       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    646    646       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    698    698       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    722    722       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    741    741       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    762    762       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    864    864       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    903    903       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    965    965       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    166    192       Missing (in isoform Short).
FT                                /FTId=VSP_005386.
FT   CONFLICT    808    808       R -> Y (IN REF. 3).
SQ   SEQUENCE   1035 AA;  114887 MW;  E207970B08296E13 CRC64;

  Query Match           27.4%;  Score 669.5;  DB 1;  Length 1035;
  Best Local Similarity   37.0%;  Pred. No. 1.2e-48;
  Matches  146;  Conservative   70;  Mismatches  146;  Indels   33;  Gaps   14;

Qy         66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
              ||||    |    ::|:   :|| |:  |||   |||| ||  |||:       : ::|
Db        652 GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 710

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
               : |   |:::|    ::   | ||  :  : ::   | |     :|:::
Db        711 IQSIWHVACAENWTTQISDDVCQLLGLGT--GNSSVPTFSTGG---GPYVNLN------- 758

Qy        181 VTALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQAS 233
               || : |: :   : |    :: |||   :|| :   :  | :||||: |    |||  :
Db        759 -TAPNGSLILTPSQQCLEDSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVA 817

Qy        234 LQFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEK 289
              | |    :|| |:::  |:::||||||   : |  |   :||   | | :|   : |:::
Db        818 LYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQ 877

Qy        290 IVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG 349
              || :  |  :|  ||||:| |   : : : |||:|||   : || |::|  :||||
Db        878 IVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQ 937

Qy        350 GDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQE 408
              |  : ||  | |||:||: |  :   |   |: :|:|||| ||||||||||||||:|||
Db        938 GSTADVLQEADVPLLSNEKCQQQMPEYN--ITENMVCAGYEAGGVDSCQGDSGGPLMCQE 995

Qy        409 RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
               | | | ||||  ||  |:|||| ||  | :||
Db        996 NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWI 1030


RESULT 10
ENTK_HUMAN
ID   ENTK_HUMAN     STANDARD;      PRT;  1019 AA.
AC   P98073;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).
GN   PRSS7 OR ENTK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Duodenum;
RX   MEDLINE=95234679; PubMed=7718557;
RA   Kitamoto Y., Veile R.A., Donis-Keller H., Sadler J.E.;
RT   "cDNA sequence and chromosomal localization of human enterokinase,
RT   the proteolytic activator of trypsinogen.";
RL   Biochemistry 34:4562-4568(1995).
RN   [2]
RP   SEQUENCE FROM N.A., AND DISEASE.
RX   MEDLINE=21606074; PubMed=11719902;
RA   Holzinger A., Maier E.M., Buck C., Mayerhofer P.U., Kappler M.,
RA   Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher A.A.;
RT   "Mutations in the proenteropeptidase gene are the molecular cause of
RT   congenital enteropeptidase deficiency.";
RL   Am. J. Hum. Genet. 70:20-25(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20289799; PubMed=10830953;
RA   Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA   Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA   Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA   Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA   Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA   Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA   Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA   Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA   Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA   Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA   Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA   Lehrach H., Reinhardt R., Yaspo M.-L.;
RT   "The DNA sequence of human chromosome 21.";
RL   Nature 405:311-319(2000).
RN   [4]
RP   SEQUENCE OF 749-1019 FROM N.A.
RC   TISSUE=Duodenum;
RX   MEDLINE=94329561; PubMed=8052624;
RA   Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.;
RT   "Enterokinase, the initiator of intestinal digestion, is a mosaic
RT   protease composed of a distinctive assortment of domains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
CC   -!- FUNCTION: Responsible for initiating activation of pancreatic
CC       proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC       A). It catalyzes the conversion of trypsinogen to trypsin which in
CC       turn activates other proenzymes including chymotrypsinogen,
CC       procarboxypeptidases, and proelastases.
CC   -!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC       trypsinogen.
CC   -!- SUBUNIT: Heterodimer of a catalytic (light) chain and a
CC       multidomain (heavy) chain linked by a disulfide bond.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Intestinal brush border.
CC   -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC       CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC   -!- DISEASE: Defects in PRSS7 are a cause of enterokinase deficiency
CC       [MIM:226200]; a life-threatening intestinal malabsorption disorder
CC       characterized by diarrhea and failure to thrive.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 2 CUB domains.
CC   -!- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 1 MAM domain.
CC   -!- SIMILARITY: Contains 1 SEA domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U09860; AAC50138.1; -.
DR   EMBL; Y19124; CAB65555.1; -.
DR   EMBL; Y19125; CAB65555.1; JOINED.
DR   EMBL; Y19126; CAB65555.1; JOINED.
DR   EMBL; Y19127; CAB65555.1; JOINED.
DR   EMBL; Y19128; CAB65555.1; JOINED.
DR   EMBL; Y19129; CAB65555.1; JOINED.
DR   EMBL; Y19130; CAB65555.1; JOINED.
DR   EMBL; Y19131; CAB65555.1; JOINED.
DR   EMBL; Y19132; CAB65555.1; JOINED.
DR   EMBL; Y19133; CAB65555.1; JOINED.
DR   EMBL; Y19134; CAB65555.1; JOINED.
DR   EMBL; Y19135; CAB65555.1; JOINED.
DR   EMBL; Y19136; CAB65555.1; JOINED.
DR   EMBL; Y19137; CAB65555.1; JOINED.
DR   EMBL; Y19138; CAB65555.1; JOINED.
DR   EMBL; Y19139; CAB65555.1; JOINED.
DR   EMBL; Y19140; CAB65555.1; JOINED.
DR   EMBL; Y19141; CAB65555.1; JOINED.
DR   EMBL; Y19142; CAB65555.1; JOINED.
DR   EMBL; Y19143; CAB65555.1; JOINED.
DR   EMBL; AL163218; CAB90392.1; -.
DR   EMBL; AL163217; CAB90389.1; -.
DR   PIR; A56318; A56318.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.156; -.
DR   Genew; HGNC:9490; PRSS7.
DR   MIM; 606635; -.
DR   MIM; 226200; -.
DR   GO; GO:0005903; C:brush border; TAS.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000998; MAM_domain.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR000082; SEA_domain.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00057; ldl_recept_a; 2.
DR   Pfam; PF00629; MAM; 1.
DR   Pfam; PF01390; SEA; 1.
DR   Pfam; PF00530; SRCR; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PRINTS; PR00020; MAMDOMAIN.
DR   SMART; SM00042; CUB; 2.
DR   SMART; SM00192; LDLa; 2.
DR   SMART; SM00137; MAM; 1.
DR   SMART; SM00200; SEA; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01180; CUB; 2.
DR   PROSITE; PS01209; LDLRA_1; 2.
DR   PROSITE; PS50068; LDLRA_2; 2.
DR   PROSITE; PS00740; MAM_1; 1.
DR   PROSITE; PS50060; MAM_2; 1.
DR   PROSITE; PS50024; SEA; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;
KW   Zymogen; Transmembrane; Repeat; Lipoprotein.
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FT   CHAIN        1    784       NON-CATALYTIC CHAIN (HEAVY CHAIN).
FT   CHAIN      785   1019       CATALYTIC CHAIN (LIGHT CHAIN).
FT   DOMAIN       1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    19     47       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                               (POTENTIAL).
FT   DOMAIN      48   1019       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      52    169       SEA.
FT   DOMAIN     182    223       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN     225    334       CUB 1.
FT   DOMAIN     342    504       MAM.
FT   DOMAIN     524    634       CUB 2.
FT   DOMAIN     641    679       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN     678    771       SRCR.
FT   DOMAIN     785   1019       SERINE PROTEASE.
FT   ACT_SITE   825    825       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   876    876       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   971    971       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   LIPID        2      2       N-myristoyl glycine (Potential).
FT   DISULFID   184    197       BY SIMILARITY.
FT   DISULFID   191    210       BY SIMILARITY.
FT   DISULFID   204    221       BY SIMILARITY.
FT   DISULFID   643    655       BY SIMILARITY.
FT   DISULFID   650    668       BY SIMILARITY.
FT   DISULFID   662    677       BY SIMILARITY.
FT   DISULFID   772    896       INTERCHAIN (BY SIMILARITY).
FT   DISULFID   810    826       BY SIMILARITY.
FT   DISULFID   910    977       BY SIMILARITY.
FT   DISULFID   941    956       BY SIMILARITY.
FT   DISULFID   967    995       BY SIMILARITY.
FT   CARBOHYD   116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   328    328       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   335    335       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   388    388       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   440    440       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   470    470       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   503    503       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   534    534       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   630    630       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   682    682       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   706    706       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   725    725       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   848    848       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   887    887       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   909    909       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   949    949       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   134    134       Q -> E (IN REF. 3).
FT   CONFLICT   732    732       S -> P (IN REF. 3).
FT   CONFLICT   754    771       SQQCLQDSLIRLQCNHKS -> RRNAKNEIDALSPIILIA
FT                               (IN REF. 3).
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  Query Match          27.2%;  Score 664.5;  DB 1;  Length 1019;
  Best Local Similarity  37.5%;  Pred. No. 3.1e-48;
  Matches  147;  Conservative   67;  Mismatches  149;  Indels   29;  Gaps   14;

Qy        67 LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
             |||   |  :  ::|::  :|: |:  |||   |:|| ||  |||        | :::
Db       637 LGIPEPCKADHFQCKNG-ECVPLVNLCDGHLHCEDGSDEADCVRFFNGTTNNNGLVRFRI 695

Qy       122 AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
             : | | |:::|    :|  |  ||  |  ||     : | :|      || : :  ||
Db       696 QSIWHTACAENWTTQISNDVCQLLGLGSGNSSK--PIFSTDG---GPFVKL-NTAPDG-- 747

Qy       182 TALHHSVYVREGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQASLQF 236
               |  :   : |    :: |||   :|| :   :  : :||||: :    |||    | :
Db       748 ---HLILTPSQQCLQDSLIRLQCNHKSCGKKLAAQDITPKIVGGSNAKEGAWPWVVGLYY 804

Qy       237 QGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEKIVY 292
             | ||| |:::  |:::||||||   | |  ||  :||   | | :|     |:::||
Db       805 GGRLLCGASLVSSDWLVSAAHCVYGRNLEPSKWTAILGLHMKSNLTSPQTVPRLIDEIVI 864

Qy       293 HSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDA 352
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Db        865 NPHYNRRRKDNDIAMMHLEFKVNYTDYIQPICLPEENQVFPPGRNCSIAGWGTVVYQGTT 924

Qy        353 SPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRL 411

Db        925 ANILQEADVPLLSNERCQQQMPEYN--ITENMICAGYEEGGIDSCQGDSGGPLMCQENNR 982

Qy        412 WKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443

Db        983 WFLAGVTSFGYKCALPNRPGVYARVSRFTEWI 1014


RESULT 11
ENTK_PIG
ID   ENTK_PIG       STANDARD;      PRT;  1034 AA.
AC   P98074;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).
GN   PRSS7 OR ENTK.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Duodenal mucosa;
RX   MEDLINE=94327548; PubMed=8051081;
RA   Matsushima M., Ichinose M., Yahagi N., Kakei N., Tsukada S.,
RA   Miki K., Kurokawa K., Tashiro K., Shiokawa K., Shinomiya K.,
RA   Umeyama H., Inoue H., Takahashi T., Takahashi K.;
RT   "Structural characterization of porcine enteropeptidase.";
RL   J. Biol. Chem. 269:19976-19982(1994).
CC   -!- FUNCTION: Responsible for initiating activation of pancreatic
CC       proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC       A). It catalyzes the conversion of trypsinogen to trypsin which in
CC       turn activates other proenzymes including chymotrypsinogen,
CC       procarboxypeptidases, and proelastases.
CC   -!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC       trypsinogen.
CC   -!- SUBUNIT: Heterotrimer of a catalytic (light) chain, a multidomain
CC       (heavy) chain, and a mini chain.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC   -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC       CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC   -!- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 2 CUB domains.
CC   -!- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 1 MAM domain.
CC   -!- SIMILARITY: Contains 1 SEA domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; D30799; BAA06459.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.156; -.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000998; MAM_domain.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR000082; SEA_domain.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00057; ldl_recept_a; 2.
DR   Pfam; PF00629; MAM; 1.
DR   Pfam; PF01390; SEA; 1.
DR   Pfam; PF00530; SRCR; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PRINTS; PR00020; MAMDOMAIN.
DR   SMART; SM00042; CUB; 2.
DR   SMART; SM00192; LDLa; 2.
DR   SMART; SM00137; MAM; 1.
DR   SMART; SM00200; SEA; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01180; CUB; 2.
DR   PROSITE; PS01209; LDLRA_1; 2.
DR   PROSITE; PS50068; LDLRA_2; 2.
DR   PROSITE; PS00740; MAM_1; 1.
DR   PROSITE; PS50060; MAM_2; 1.
DR   PROSITE; PS50024; SEA; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;
KW   Zymogen; Transmembrane; Repeat; Lipoprotein.
FT   CHAIN        52    117       NON-CATALYTIC M CHAIN (MINI CHAIN).
FT   CHAIN       118    799       NON-CATALYTIC H CHAIN (HEAVY CHAIN).
FT   CHAIN       800   1034       CATALYTIC L CHAIN (LIGHT CHAIN).
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     19     47       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       48   1034       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       52    169       SEA.
FT   DOMAIN      197    238       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN      240    349       CUB 1.
FT   DOMAIN      357    519       MAM.
FT   DOMAIN      539    649       CUB 2.
FT   DOMAIN      656    694       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN      693    786       SRCR.
FT   DOMAIN      800   1034       SERINE PROTEASE.
FT   ACT_SITE    840    840       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    891    891       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    986    986       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   LIPID         2      2       N-myristoyl glycine (Potential).
FT   DISULFID    199    212       BY SIMILARITY.
FT   DISULFID    206    225       BY SIMILARITY.
FT   DISULFID    219    236       BY SIMILARITY.
FT   DISULFID    658    670       BY SIMILARITY.
FT   DISULFID    665    683       BY SIMILARITY.
FT   DISULFID    677    692       BY SIMILARITY.
FT   DISULFID    787    911       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    825    841       BY SIMILARITY.
FT   DISULFID    925    992       BY SIMILARITY.
FT   DISULFID    956    971       BY SIMILARITY.
FT   DISULFID    982   1010       BY SIMILARITY.
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    194    194       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    343    343       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    350    350       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    403    403       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    455    455       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    485    485       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    518    518       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    549    549       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    645    645       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    697    697       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    701    701       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    721    721       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    740    740       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    761    761       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    804    804       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    863    863       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    902    902       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    964    964       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1034 AA;  114776 MW;  0388C64CF64CC368 CRC64;

  Query Match             27.2%;  Score 663.5;  DB 1;  Length 1034;
  Best Local Similarity   37.8%;  Pred. No. 3.9e-48;
  Matches  149;  Conservative   65;  Mismatches  147;  Indels   33;  Gaps   14;

Qy         67 LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
              |||   |    ::| :  :|: |:  ||| | |||| ||  |||        : ::|
Db        652 LGIPEPCKEDNFQCENG-ECVLLVNLCDGFSHCKDGSDEAHCVRFLNGTANNSGLVQFRI 710

Qy        122 AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
               : | | |:::|    ::  |  ||  :  ||     ||  |     || ::
Db        711 QSIWHTACAENWTTQTSDDVCQLLGLGTGNSSMPF-FSSGGG----PFVKLN-------- 757

Qy        182 TALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQASL 234
              || : |: :   | |    :: |||   :|| :   :  | :|||| |    ||| :|
Db        758 TAPNGSLILTASEQCFEDSLILLQCNHKSCGKKQVAQEVSPKIVGGNDSREGAWPWVVAL 817

Qy        235 QFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEKI 290
               : |  ||| |:::  |:::|||||    | |  |   :||   | | :|   : |:::|
Db        818 YYNGQLLCGASLVSRDWLVSAAHCVYGRNLEPSKWKAILGLHMTSNLTSPQIVTRLIDEI 877

Qy        291 VYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGG 350
              | :  |  :|  :|||:| |   : : : |||:|||   : || |::|  :|||     |
Db        878 VINPHYNRRRKDSDIAMMHLEFKVNYTDYIQPICLPEENQVFPPGRICSIAGWGKVIYQG 937

Qy        351 DASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQER 409
               : :|  | |||:||: | :  |  |: :|:|||| ||:|||||||'|||:| |
Db        938 SPADILQEADVPLLSNEKCQQQMPEYN--ITENMMCAGYEEGGIDSCQGDSGGPLMCLEN 995

Qy        410 RLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
                | | | |||| ||  |:|||| ||  | :||
Db        996 NRWLLAGVTSFGYQCALPNRPGVYARVPKFTEWI 1029


RESULT 12
HEPS_MOUSE
ID   HEPS_MOUSE     STANDARD;      PRT;   436 AA.
AC   O35453; Q9CW97;
DT   15-JUL-1998 (Rel. 36, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Serine protease hepsin (EC 3.4.21.-).
GN   HPN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Liver;
RX   MEDLINE=98058912; PubMed=9395459;
RA   Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.;
RT   "Identification and cloning of the membrane-associated serine
RT   protease, hepsin, from mouse preimplantation embryos.";
RL   J. Biol. Chem. 272:31315-31320(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=99339944; PubMed=10411637;
RA   Kawamura S., Kurachi S., Deyashiki Y., Kurachi K.;
RT   "Complete nucleotide sequence, origin of isoform and functional
RT   characterization of the mouse hepsin gene.";
RL   Eur. J. Biochem. 262:755-764(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Plays an essential role in cell growth and maintenance
CC       of cell morphology.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=1a;
CC         IsoId=O35453-1; Sequence=Displayed;
CC         Note=Minor isoform;
CC       Name=2; Synonyms=2a;
CC         IsoId=O35453-2; Sequence=VSP_007232;
CC         Note=Major isoform;
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to
CC       frameshifts in positions 155, 191 and 233.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF030065; AAB84221.1; -.
DR   EMBL; AK002694; BAB22289.2; ALT_FRAME.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.224; -.
DR   MGD; MGI:1196620; Hpn.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW   Alternative splicing.
FT   CHAIN         1    181       SERINE PROTEASE HEPSIN, NON-CATALYTIC
FT                                CHAIN (POTENTIAL).
FT   CHAIN       182    436       SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
FT                                (POTENTIAL).
FT   DOMAIN       21     36       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     37     63       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       64    436       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      182    436       SERINE PROTEASE.
FT   ACT_SITE    222    222       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    276    276       CHARGE RELAY SYSTEM (BY SIMILARITY).
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FT   ACT_SITE    372    372       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID    172    296       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    207    223       BY SIMILARITY.
FT   DISULFID    341    357       BY SIMILARITY.
FT   DISULFID    368    400       BY SIMILARITY.
FT   CARBOHYD    131    131       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     25     44       Missing (in isoform 2).
FT                                /FTId=VSP_007232.
FT   CONFLICT     85     85       L -> F (IN REF. 2 AND 3).
FT   CONFLICT    204    204       T -> Y (IN REF. 3).
FT   CONFLICT    214    214       G -> R (IN REF. 3).
FT   CONFLICT    228    229       NR -> ET (IN REF. 3).
FT   CONFLICT    264    264       P -> L (IN REF. 3).
FT   CONFLICT    281    281       H -> N (IN REF. 3).
SQ   SEQUENCE   436 AA;  46787 MW;  4A0993148C620BD0 CRC64;

  Query Match           27.0%;  Score 659.5;  DB 1;  Length 436;
  Best Local Similarity   38.6%;  Pred. No. 3.1e-48;
  Matches  136;  Conservative   49;  Mismatches  128;  Indels   39;  Gaps    7;

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSID------- 173
              |  :|: :||       | : | ::||   ::   | | :        |  :|
Db         88 TEGTWRLLCSSRSNARVAGLGCEEMGFLRALAHSELDVRTAGANGTSGFFCVDEGGLPLA 147

Qy        174 -HLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQA 232
               ||  | ::            |  |  :|  |  || |:    |||||  | | :||||
Db        148 QRLL--DVISVC--------DCPRGRFLTATCQDCGRRKLPVDRIVGGQDSSLGRWPWQV 197

Qy        233 SLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK------SWTIQVGLVSLLDNPAPSHL 286
              ||:: | ||||||:::  |::|||||       |:      | :  | |:       |
Db        198 SLRYDGTHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRVFAGAVARTSPHAVQLG 252

Qy        287 VEKIVYHSKYKPKR------LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWT 340
              |: ::||  | | |        |||||: |:  |   | ||||||| : :   |||||
Db        253 VQAVIYHGGYLPFRDPTIDENSNDIALVHLSSSLPLTEYIQPVCLPAAGQALVDGKVCTV 312

Qy        341 SGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDS 400
              :|||.|:  |  : ||  | ||:|||::||  | ||  | | | ||||  ||:|:|||||
Db        313 TGWGNTQFYGQQAMVLQEARVPIISNEVCNSPDFYGNQIKPKMFCAGYPEGGIDACQGDS 372

Qy        401 GGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              ||| ||::       |:| |  |:| |||   ||||||:|| | :|| : ::
Db        373 GGPFVCEDSISGTSRWRLCGIVSWGTGCALARKPGVYTKVTDFREWIFKAIK 424


RESULT 13
TMS4_HUMAN
ID   TMS4_HUMAN     STANDARD;      PRT;   437 AA.
AC   Q9NRS4; Q9NZA5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine
DE   protease 2) (MT-SP2).
GN   TMPRSS4 OR TMPRSS3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreatic carcinoma;
RX   MEDLINE=20283276; PubMed=10825129;
RA   Wallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B.,
RA   Iwamura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.;
RT   "A novel transmembrane serine protease (TMPRSS3) overexpressed in
RT   pancreatic cancer.";
RL   Cancer Res. 60:2602-2606(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.;
RT   "MT-SP2, a novel type II membrane serine protease expressed in
RT   trachea, colon, and small intestine: identification, cloning, and
RT   chromosomal localization.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Probable protease. Seems to be capable of activating
CC       ENaC (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: High levels in pancreatic, gastric, colorectal
CC       and ampullary cancer. Very weak expression in normal
CC       gastrointestinal and urogenital tract.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF179224; AAF74526.1; -.
DR   EMBL; AF216312; AAF31436.1; -.
DR   EMBL; BC011703; AAH11703.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.034; -.
DR   Genew; HGNC:11878; TMPRSS4.
DR   MIM; 606565; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; FALSE_NEG.
DR   PROSITE; PS50068; LDLRA_2; FALSE_NEG.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor.
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FT   DOMAIN        1     32       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     33     53       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       54    437       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       61     93       LDL-RECEPTOR CLASS A.
FT   DOMAIN       94    204       SRCR.
FT   DOMAIN      205    437       SERINE PROTEASE.
FT   ACT_SITE    245    245       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    290    290       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    387    387       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE        204    205       CLEAVAGE (POTENTIAL).
FT   DISULFID     64     83       BY SIMILARITY.
FT   DISULFID     77     92       BY SIMILARITY.
FT   DISULFID    127    183       BY SIMILARITY.
FT   DISULFID    140    193       BY SIMILARITY.
FT   DISULFID    196    310       BY SIMILARITY.
FT   DISULFID    230    246       BY SIMILARITY.
FT   DISULFID    356    372       BY SIMILARITY.
FT   DISULFID    383    410       BY SIMILARITY.
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      1     31       MLQDPDSDQPLNSLDVKPLRKPRIPMETFRK -> MSNPCA
FT                                NPVSPWRPSES (IN REF. 2).
SQ   SEQUENCE   437 AA;  48204 MW;  351B2FD4A8657B12 CRC64;
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Query Match 26.9%; Score 658; DB 1; Length 437;
Best Local Similarity 35.7%; Pred. No. 4.1e-48;
Matches 158; Conservative 75; Mismatches 146; Indels 64; Gaps 18;

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Qy         44 LPLKFFPIIVIGIIALILALA------IGLGIHFDCSGKYRCRSSFKC---IELIAR--- 91
Db         24 IPMETFRKVGIPIIIALLSLASIIIVVVLIKVILD---KY----YFLCGQPLHFIPRKQL 76

Qy         92 CDGVSDCKDGEDEYRC-----------VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYA 138
Db         77 CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA 136

Qy        139 NVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREG---CA 195
Db        137 ETACRQMGYSS------------KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCL 184

Qy        196 SGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITA 255
Db        185 SGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 243

Qy        256 AHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYKPKRLGNDIALMK 309
Db        244 AHCFRKHTDVF---NWKVRAGSDKL--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMK 295

Qy        310 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGAT-EDGGDASPVLNHAAVPLISNKI 368
Db        296 LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR 355

Qy        369 CNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVN 428
Db        356 CNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPS 414

Qy        429 KPGVYTRVTSFLDWIHEQMERDL 451
Db        415 TPGVYTKVSAYLNWIYNVWKAEL 437
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RESULT 14
HEPS_RAT
ID   HEPS_RAT       STANDARD;      PRT;   416 AA.
AC   Q05511;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Serine protease hepsin (EC 3.4.21.-).
GN   HPN.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93305733; PubMed=8318546;
RA   Farley D., Reymond F., Nick H.;
RT   "Cloning and sequence analysis of rat hepsin, a cell surface serine
RT   proteinase.";
RL   Biochim. Biophys. Acta 1173:350-352(1993).
CC   -!- FUNCTION: Plays an essential role in cell growth and maintenance
CC       of cell morphology.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X70900; CAA50256.1; -.
DR   PIR; S33777; S33777.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.224; -.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor.
FT   CHAIN         1    161       SERINE PROTEASE HEPSIN, NON-CATALYTIC
FT                                CHAIN (POTENTIAL).
FT   CHAIN       162    416       SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
FT                                (POTENTIAL).
FT   DOMAIN        1     16       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     17     43       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       44    416       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      162    416       SERINE PROTEASE.
FT   ACT_SITE    202    202       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    256    256       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    352    352       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID    152    276       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    187    203       BY SIMILARITY.
FT   DISULFID    321    337       BY SIMILARITY.
FT   DISULFID    348    380       BY SIMILARITY.
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   416 AA;  44926 MW;  E5A9F8FA9550E180 CRC64;
```

Query Match 26.8%; Score 654.5; DB 1; Length 416;
Best Local Similarity 35.3%; Pred. No. 7.7e-48;
Matches 146; Conservative 61; Mismatches 156; Indels 51; Gaps 10;

```
Qy         60 ILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQV 119
Db         17 VAALTVGTLLFLTGIG----AASWAIVTILLR-------SDQEPLYQVQLSPGDSRLLVL 65

Qy        120 -FTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSID----- 173
Db         66 DKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAHSELDVRTAGANGTSGFFCVDEGGLP 125

Qy        174 ---HLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPW 230
Db        126 LAQRLL--DVISVC--------DCPRGRFLTATCQDCGRRKLPVDRIVGGQDSSLGRWPW 175
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```
Qy        231 QASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK------SWTIQVGLVSLLDNPAPS 284
              | ||:: | |||||||:::  |::|||||      |:      | :  | |:      |
Db        176 QVSLRYDGTHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRVFAGAVARTSPHAVQ 230

Qy        285 HLVEKIVYHSKYKPKR------LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVC 338
                |: ::||  | | |        |||||: |:  |   | |||||| : :   |||||
Db        231 LGVQAVIYHGGYLPFRDPTIDENSNDIALVHLSSSLPLTEYIQPVCLPAAGQALVDGKVC 290

Qy        339 WTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG 398
                :||| |:  |  : ||  | ||:|||::||  | ||  | | | ||||  ||:|:|||
Db        291 TVTGWGNTQFYGQQAVVLQEARVPIISNEVCNSPDFYGNQIKPKMFCAGYPEGGIDACQG 350

Qy        399 DSGGPLVCQER----RLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              ||||  ||::|       |:| |  |:| |||   ||||||:|  | :|| : ::
Db        351 DSGGHFVCEDRISGTSRWRLCGIVSWGTGCALARKPGVYTKVIDFREWIFQAIK 404


RESULT 15
ENTK_MOUSE
ID   ENTK_MOUSE     STANDARD;      PRT;  1069 AA.
AC   P97435;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Enteropeptidase (EC 3.4.21.9) (Enterokinase).
GN   PRSS7 OR ENTK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Duodenum;
RX   MEDLINE=98147142; PubMed=9486188;
RA   Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., Sadler J.E.;
RT   "Structure of murine enterokinase (enteropeptidase) and expression in
RT   small intestine during development.";
RL   Am. J. Physiol. 274:G342-G349(1998).
CC   -!- FUNCTION: Responsible for initiating activation of pancreatic
CC       proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC       A). It catalyzes the conversion of trypsinogen to trypsin which in
CC       turn activates other proenzymes including chymotrypsinogen,
CC       procarboxypeptidases, and proelastases (By similarity).
CC   -!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC       trypsinogen.
CC   -!- SUBUNIT: Heterodimer of a catalytic (light) chain and a
CC       multidomain (heavy) chain linked by a disulfide bond (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC   -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC       CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
CC   -!- SIMILARITY: Contains 2 CUB domains.
CC   -!- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 1 MAM domain.
CC   -!- SIMILARITY: Contains 1 SEA domain.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U73378; AAB37317.1; -.
DR   HSSP; Q07954; 1CR8.
DR   MEROPS; S01.156; -.
DR   MGD; MGI:1197523; Prss7.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000998; MAM_domain.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009020; Protease_inhib.
DR   InterPro; IPR000082; SEA_domain.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00057; ldl_recept_a; 2.
DR   Pfam; PF00629; MAM; 1.
DR   Pfam; PF01390; SEA; 1.
DR   Pfam; PF00530; SRCR; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PRINTS; PR00020; MAMDOMAIN.
DR   SMART; SM00042; CUB; 2.
DR   SMART; SM00192; LDLa; 2.
DR   SMART; SM00137; MAM; 1.
DR   SMART; SM00200; SEA; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01180; CUB; 2.
DR   PROSITE; PS01209; LDLRA_1; 2.
DR   PROSITE; PS50068; LDLRA_2; 2.
DR   PROSITE; PS00740; MAM_1; 1.
DR   PROSITE; PS50060; MAM_2; 1.
DR   PROSITE; PS50024; SEA; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Signal-anchor; Glycoprotein; Hydrolase; Serine protease; Zymogen;
KW   Transmembrane; Repeat.
FT   CHAIN         1    829       NON-CATALYTIC CHAIN (HEAVY CHAIN).
FT   CHAIN       830   1069       CATALYTIC CHAIN (LIGHT CHAIN).
FT   DOMAIN        1     18       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     19     47       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       48   1069       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       52    169       SEA.
FT   DOMAIN      227    268       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN      270    379       CUB 1.
FT   DOMAIN      387    549       MAM.
FT   DOMAIN      569    679       CUB 2.
FT   DOMAIN      686    724       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN      723    816       SRCR.
FT   DOMAIN      830   1069       SERINE PROTEASE.
FT   ACT_SITE    874    874       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    925    925       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   1021   1021       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID    229    242       BY SIMILARITY.
FT   DISULFID    236    255       BY SIMILARITY.
FT   DISULFID    249    266       BY SIMILARITY.
FT   DISULFID    688    700       BY SIMILARITY.
FT   DISULFID    695    713       BY SIMILARITY.
FT   DISULFID    707    722       BY SIMILARITY.
FT   DISULFID    817    945       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    859    875       BY SIMILARITY.
FT   DISULFID    959   1027       BY SIMILARITY.
FT   DISULFID    991   1006       BY SIMILARITY.
FT   DISULFID   1017   1045       BY SIMILARITY.
FT   CARBOHYD    147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    212    212       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    373    373       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    380    380       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    433    433       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    515    515       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    579    579       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    675    675       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    727    727       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

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FT   CARBOHYD    751    751       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    770    770       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    791    791       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    897    897       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    936    936       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    999    999       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1069 AA;  118735 MW;  E62549E463743C3D CRC64;

  Query Match           26.6%;  Score 651;  DB 1;  Length 1069;
  Best Local Similarity   37.4%;  Pred. No. 4.6e-47;
  Matches  151;  Conservative   65;  Mismatches  142;  Indels   46;  Gaps   17;

Qy         67 LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
              |||    |   :::|:    || |   ||     |:|| ||  |||         | ::|
Db        682 LGIPEPCQDDEFQCKDG-NCIPLGNLCDSYPHCRDGSDEASCVRFLNGTRSNNGLVQFNI 740

Qy        122 AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
             : |   |:::|    :|  |  ||  |  :: :: :||  |      || ::
Db        741 HSIWHIACAENWTTQISNEVCHLLGLGS--ANSSMPISSTGG---GPFVRVNQ------- 788

Qy        182 TALHHSVYVREG--CASGHVVTLQCT--ACGHRR---GYSSRIVGGNMSLLSQWPWQASL 234
             | : |: :      |:   :: |||   :|| ::     | :|||: :    ||| :|
Db        789 -APNGSLILTPSLQCSQDSLILLQCNHKSCGEKKVTQKVSPKIVGGSDAQAGAWPWVVAL 847

Qy        235 QFQGYH--------LCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-A 282
                ||         ||| |:::  |:::||||||   | |  ||  :||   | | :|
Db        848 ----YHRDRSTDRLLCGASLVSSDWLVSAAHCVYRRNLDPTRWTAVLGLHMQSNLTSPQV 903

Qy        283 PSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSG 342
             :|::|| :  |  :|  ||||:| |   : : : |||:|||   : |  |: |  :|
Db        904 VRRVVDQIVINPHYDRRRKVNDIAMMHLEFKVNYTDYIQPICLPEENQIFIPGRTCSIAG 963

Qy        343 WGATE-DGGDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDS 400
             ||  : : |    ||  | ||||||: |  :   |   |: ||:|||| ||:|||||||
Db        964 WGYDKINAGSTVDVLKEADVPLISNEKCQQQLPEYN--ITESMICAGYEEGGIDSCQGDS 1021

Qy        401 GGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIH 444
             ||||:|||   | ||| |||: ||  | |||| ||: |::|||
Db       1022 GGPLMCQENNRWFLVGVTSFGVQCALPNHPGVYVRVSQFIEWIH 1065


Search completed: May  5, 2004, 15:47:20
Job time : 19 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 5, 2004, 15:40:30 ; Search time 60 Seconds
(without alignments)
2133.234 Million cell updates/sec

Title: US-09-846-512-2
Perfect score: 2443
Sequence: 1 MGENDPPAVEAPFSFRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2443	100.0	453	4	AAU29055	Aau29055 Human PRO
2	2443	100.0	453	4	AAE06935	Aae06935 Human mem
3	2443	100.0	453	5	AAO18402	Aao18402 Human ser
4	2443	100.0	453	5	ABJ05565	Abj05565 Breast ca
5	2443	100.0	453	5	AAE23020	Aae23020 Human try
6	2443	100.0	453	6	ABU58431	Abu58431 Human PRO
7	2443	100.0	453	6	ABU87979	Abu87979 Novel hum
8	2443	100.0	453	6	ABU84294	Abu84294 Human sec
9	2443	100.0	453	6	ABR66168	Abr66168 Human sec
10	2443	100.0	453	6	ABR65558	Abr65558 Human sec
11	2443	100.0	453	6	ABU99498	Abu99498 Human sec
12	2443	100.0	453	6	ABU82737	Abu82737 Human PRO
13	2443	100.0	453	6	ABU89858	Abu89858 Novel hum
14	2443	100.0	453	6	ABR58549	Abr58549 Human can
15	2443	100.0	453	6	ABR68107	Abr68107 Human sec
16	2443	100.0	453	6	ABU96160	Abu96160 Novel hum
17	2443	100.0	453	6	ABU92591	Abu92591 Human sec
18	2443	100.0	453	6	ABO08668	Abo08668 Human sec
19	2443	100.0	453	6	ABO02720	Abo02720 Human sec
20	2443	100.0	453	6	ABR74874	Abr74874 Human sec
21	2443	100.0	453	6	ABR94636	Abr94636 Human sec
22	2443	100.0	453	6	ABO25196	Abo25196 Novel hum
23	2443	100.0	453	6	ABU85609	Abu85609 Human PRO
24	2443	100.0	453	6	ABU98769	Abu98769 Novel hum
25	2443	100.0	453	6	ABU97984	Abu97984 Novel hum
26	2443	100.0	453	6	ABU91690	Abu91690 Novel hum
27	2443	100.0	453	6	ABU72202	Abu72202 Novel hum
28	2443	100.0	453	6	ABU89383	Abu89383 Human PRO
29	2443	100.0	453	6	ABU86224	Abu86224 Human sec
30	2443	100.0	453	6	ABU67437	Abu67437 Human sec
31	2443	100.0	453	6	ABU80465	Abu80465 Human PRO
32	2443	100.0	453	6	ABR99383	Abr99383 Human sec
33	2443	100.0	453	6	ABR98773	Abr98773 Human sec
34	2443	100.0	453	6	ABO16296	Abo16296 Human sec
35	2443	100.0	453	6	ABR92196	Abr92196 Human sec
36	2443	100.0	453	6	ABO18837	Abo18837 Human sec
37	2443	100.0	453	6	ABR78258	Abr78258 Human sec
38	2443	100.0	453	6	ABU56617	Abu56617 Lung canc
39	2443	100.0	453	6	ABU84994	Abu84994 Novel hum
40	2443	100.0	453	6	ABO00133	Abo00133 Novel hum
41	2443	100.0	453	6	ABO11465	Abo11465 Human sec
42	2443	100.0	453	6	ABO02110	Abo02110 Human sec
43	2443	100.0	453	6	ABU88684	Abu88684 Novel hum
44	2443	100.0	453	6	ABU83379	Abu83379 Human sec
45	2443	100.0	453	6	ABO06180	Abo06180 Novel hum

ALIGNMENTS

RESULT 1
AAU29055
ID AAU29055 standard; protein; 453 AA.
XX
AC AAU29055;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #32.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.

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PR   25-APR-2000; 2000US-0199550P.
PR   25-APR-2000; 2000US-0199654P.
PR   03-MAY-2000; 2000US-0201516P.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI   Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS45956.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumors, such as prostate and breast tumors, in mammals and to
PT   screen for modulators of the compounds.
XX
PS   Claim 11; Fig 64; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders
XX
SQ   Sequence 453 AA;

  Query Match             100.0%;  Score 2443;  DB 4;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-188;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||||||||||||||||||||||
Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453


RESULT 2
AAE06935
ID   AAE06935 standard; protein; 453 AA.
XX
AC   AAE06935;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human membrane-type serine protease (MTSP) 6.
XX
KW   Human; transmembrane serine protease; membrane-type serine protease;
KW   MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic;
KW   lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          48. .68
FT                   /label= Transmembrane_domain
FT   Domain          72. .108
FT                   /label= LDLRa_domain
FT                   /note= "LDL receptor domain class a"
FT   Domain          109. .205
FT                   /label= SR_domain
FT                   /note= "Scavenger receptor Cys-rich domain"
FT   Domain          216. .443
FT                   /note= "Trypsin-like serine protease domain"
FT   Cleavage-site   216. .217
FT   Domain          217. .443
FT                   /label= Protease_domain
FT   Misc-difference 324
FT                   /note= "Unpaired cysteine"
XX
PN   WO200157194-A2.
XX
PD   09-AUG-2001.
XX
PF   02-FEB-2001; 2001WO-US003471.
XX
PR   03-FEB-2000; 2000US-0179982P.
PR   18-FEB-2000; 2000US-0183542P.
PR   22-JUN-2000; 2000US-0213124P.
PR   26-JUL-2000; 2000US-0220970P.
PR   08-SEP-2000; 2000US-00657986.
PR   22-SEP-2000; 2000US-0234840P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL, Ong EO, Yeh J;
XX
DR   WPI; 2001-488877/53.
DR   N-PSDB; AAD13118.
XX
PT   Novel single chain polypeptide comprising protease domain of type-II
PT   membrane-type serine protease or its catalytically active portion useful
PT   for treating and preventing cancer and tumor.
XX
PS   Claim 128; Page 214-215; 256pp; English.
XX
CC   The invention relates to transmembrane serine proteases and their
CC   corresponding nucleotides and the protease domain of a type-II membrane-
```

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CC   type serine protease (MTSP). MTSP is useful for identifying compounds
CC   that modulate or inhibits its proteolytic activity and for formulating a
CC   medicament for treating neoplastic disease. MTSP and its corresponding
CC   nucleotides are useful in preventing or treating tumours or cancers such
CC   as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in
CC   diagnostics and in hybridisation assays. MTSP is useful as a diagnostic
CC   marker for tumour development, growth and/or progression and as
CC   immunogens to generate antibodies that specifically bind to it. MTSP DNA
CC   is useful in a yeast two-hybrid system and in gene therapy. The present
CC   sequence is human MTSP6 protein
XX
SQ   Sequence 453 AA;

  Query Match             100.0%;  Score 2443;  DB 4;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-188;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||||||||||||||||||||||
Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453


RESULT 3
AAO18402
ID   AAO18402 standard; protein; 453 AA.
XX
AC   AAO18402;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Human serine protease MP493.
XX
KW   Human; serine protease; MP493; cancer; kidney disease; lung disease;
KW   protein coordinate data; cytostatic; antiasthmatic; antiallergic;
KW   antiinflammatory; virucide; immunomodulator.
XX
OS   Homo sapiens.
XX
PN   WO200259295-A1.
XX
PD   01-AUG-2002.
XX
PF   23-JAN-2002; 2002WO-JP000465.
XX
PR   23-JAN-2001; 2001JP-00014963.
XX
PA   (MOCH ) MOCHIDA PHARM CO LTD.
XX
PI   Nakamura Y,  Sugano S,  Matsusue T,  Okamoto A,  Okawa K;
XX
DR   WPI; 2002-566849/60.
DR   N-PSDB; AAL48490.
XX
PT   Transmembrane serine protease MP493 for diagnosis of and developing drugs
PT   for cancer, kidney diseases and lung diseases e.g. asthma, allergy,
PT   bronchitis, pneumonectasis, pancreatitis and nephritis.
XX
PS   Claim 3; Page 155-156; 163pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of a
CC   human serine protease designated MP493. The sequences can be used in the
CC   diagnosis of and development of drugs for treating cancer, kidney and
CC   lung diseases, for example asthma, allergy, bronchitis, pneumonectasis,
CC   viral diseases, shock, multiple organ failure, pancreatitis and
CC   nephritis. The present sequence is the protein of the invention
XX
SQ   Sequence 453 AA;

  Query Match             100.0%;  Score 2443;  DB 5;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-188;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||||||||||||||||||||||
Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453


RESULT 4
ABJ05565
ID   ABJ05565 standard; protein; 453 AA.
XX
AC   ABJ05565;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Breast cancer-associated protein 30.
XX
KW   Breast cancer; breast cancer-associated gene sequence; drug development;
KW   pharmacogenetics; biosensor development.
XX
```

OS Unidentified.
XX
PN WO200259377-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002242.
XX
PR 24-JAN-2001; 2001US-0263965P.
PR 02-FEB-2001; 2001US-0265928P.
PR 09-APR-2001; 2001US-00829472.
PR 09-APR-2001; 2001US-0282698P.
PR 04-MAY-2001; 2001US-0288590P.
PR 29-MAY-2001; 2001US-0294443P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Mack DH, Gish KC, Afar D;
XX
DR WPI; 2002-583738/62.
DR N-PSDB; ABT07722.
XX
PT Detecting a breast cancer-associated transcript in a patient's cell,
PT useful for diagnosing breast cancer, comprises contacting a biological
PT sample with a polynucleotide that selectively hybridizes with breast
PT cancer nucleic acids.
XX
PS Disclosure; Page 373; 414pp; English.
XX
CC The invention comprises a method of detecting a breast cancer-associated
CC transcript in a cell from a patient. The method of the invention involves
CC contacting a biological sample from the patient with a nucleotide that
CC hybridises to one of the 69 breast cancer-associated gene sequences shown
CC in the specification. The method of the invention is useful in the
CC diagnosis or prognosis of breast cancer, and for detecting genes that are
CC up or down-regulated in breast cancer cells. Genes identified by the
CC method of the invention can be used in diagnostic purposes and also as
CC targets for screening for therapeutic compounds that modulate breast
CC cancer (e.g. hormones or antibodies). Identification of genes that are
CC over or under expressed in breast cancer can additionally provide high-
CC resolution, high-sensitivity datasets which can be used in the areas of
CC diagnostics, therapeutics, drug development, pharmacogenetics, protein
CC structure and biosensor development. Amino acid sequences ABJ05536 -
CC ABJ05604 represent the proteins encoded by the 69 breast cancer-
CC associated genes of the invention
XX
SQ Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 5; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.8e-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||||||||||||||||||||||
Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
```

RESULT 5
AAE23020
ID AAE23020 standard; protein; 453 AA.
XX
AC AAE23020;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human trypsin family member, 14094 protein #1.
XX
KW Human; 14094 protein; trypsin family; proliferation; tumour; carcinoma;
KW metastatic lesion; cancer; lung; breast; ovarian; liver; colon; sarcoma;
KW signal transduction; apoptosis; necrosis; cytostatic; enzyme.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .47
FT		/note= "Non-transmembrane region"
FT	Modified-site	14. .16
FT		/note= "Protein kinase C phosphorylation site"
FT	Domain	48. .69
FT		/note= "Transmembrane domain"
FT	Region	70. .453
FT		/note= "Non-transmembrane region"
FT	Domain	71. .109
FT		/note= "Low-density lipoprotein (LDL) receptor domain
FT		class A"
FT	Modified-site	74. .76
FT		/note= "Protein kinase C phosphorylation site"
FT	Modified-site	82. .84
FT		/note= "Protein kinase C phosphorylation site"
FT	Modified-site	94. .99
FT		/note= "N-myristylation site"
FT	Modified-site	99. .105
FT		/note= "Tyrosine kinase phosphorylation site"
FT	Domain	110. .205
FT		/note= "Scavenger receptor cysteine-rich domain"
FT	Modified-site	111. .116
FT		/note= "N-myristylation site"
FT	Modified-site	124. .126
FT		/note= "Protein kinase C phosphorylation site"
FT	Modified-site	159. .162
FT		/note= "Casein kinase II phosphorylation site"
FT	Modified-site	193. .198
FT		/note= "N-myristylation site"
FT	Modified-site	214. .216
FT		/note= "Protein kinase C phosphorylation site"
FT	Domain	216. .443
FT		/note= "Trypsin domain"
FT	Region	216. .220
FT		/note= "Proteolytic activator site"
FT	Modified-site	219. .224
FT		/note= "N-myristylation site"
FT	Modified-site	221. .224
FT		/note= "N-glycosylation site"
FT	Disulfide-bond	242. .258
FT	Region	253. .258
FT		/note= "Matches PS00134"
FT	Modified-site	276. .279
FT		/note= "Casein kinase II phosphorylation site"

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FT   Modified-site   302. .307
FT                   /note= "N-myristylation site"
FT   Modified-site   315. .318
FT                   /note= "Casein kinase II phosphorylation site"
FT   Disulfide-bond  338. .406
FT   Modified-site   341. .344
FT                   /note= "Glycosaminoglycan attachment site"
FT   Modified-site   365. .367
FT                   /note= "Protein kinase C phosphorylation site"
FT   Disulfide-bond  369. .385
FT   Modified-site   391. .396
FT                   /note= "N-myristylation site"
FT   Disulfide-bond  396. .424
FT   Region          398. .402
FT                   /note= "Matches PS00135"
FT   Modified-site   421. .426
FT                   /note= "N-myristylation site"
FT   Modified-site   438. .441
FT                   /note= "Casein kinase II phosphorylation site"
XX
PN   WO200183781-A2.
XX
PD   08-NOV-2001.
XX
PF   30-APR-2001; 2001WO-US013903.
XX
PR   28-APR-2000; 2000US-0200621P.
PR   08-AUG-2000; 2000US-00633300.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyers R,  Macbeth KJ;
XX
DR   WPI; 2002-147444/19.
DR   N-PSDB; AAD36726.
XX
PT   Novel polypeptide, 14094, which is a human trypsin family member useful
PT   for treating and preventing a disorder such as cancer of the lung,
PT   breast, ovary, liver and colon.
XX
PS   Claim 8; Page 113; 140pp; English.
XX
CC   The invention relates to an isolated polypeptide, designated 14094, which
CC   is a human trypsin family member. The invention is especially useful in
CC   screening assays such as those to identify compounds that modulate their
CC   activity or expression. The compound is used to inhibit proliferation, or
CC   induce the killing, of a 14094-expressing hyperproliferative cell (such
CC   as that found in a solid tumour, a soft tissue tumour, or a metastatic
CC   lesion, preferably a cancer selected from a sarcoma, a carcinoma, and an
CC   adenocarcinoma where the cancer is selected from lung cancer, breast
CC   cancer, ovarian cancer, liver cancer and colon cancer). The compound may
CC   be used to treat or prevent a disorder characterised by aberrant cellular
CC   proliferation or differentiation of a 14094-expressing cell such as that
CC   above, where the subject is a mammal, preferably a human. The compound
CC   may be selected from a peptide, a phosphopeptide, a small organic
CC   molecule, a small inorganic molecule and an antibody to modulate 14094 or
CC   an antisense, a ribozyme, or a triple helix molecule for modulation of
CC   14094 DNA. Preferably, (for modulation of the protein) the compound is an
CC   antibody conjugated to a therapeutic moiety selected from a cytotoxin, a
CC   cytotoxic agent and a radioactive metal ion. In addition, the compound
CC   may be administered in combination with a cytotoxic agent. The cytotoxic
CC   agent may be selected from an antimicrotubule agent, a topoisomerase I
CC   inhibitor, a topoisomerase II inhibitor, a mitotic inhibitor, an
CC   antimetabolite, an alkylating agent, an intercalating agent, an agent
CC   capable of interfering with signal transduction pathway, an agent that
CC   promotes apoptosis or necrosis and radiation. The present sequence is
CC   human 14094 protein
XX
SQ   Sequence 453 AA;

  Query Match             100.0%;  Score 2443;  DB 5;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-188;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||||||||||||||||||||||
Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453


RESULT 6
ABU58431
ID   ABU58431 standard; protein; 453 AA.
XX
AC   ABU58431;
XX
DT   15-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #32.
XX
KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027272-A1.
XX
PD   06-FEB-2003.
XX
PF   21-JUN-2002; 2002US-00176492.
XX
PR   18-SEP-1997;   97US-0059263P.
PR   18-SEP-1997;   97US-0059266P.
PR   17-OCT-1997;   97US-0062250P.
PR   21-OCT-1997;   97US-0063486P.
PR   24-OCT-1997;   97US-0063120P.
PR   24-OCT-1997;   97US-0063121P.
PR   28-OCT-1997;   97US-0063540P.
PR   28-OCT-1997;   97US-0063541P.
PR   28-OCT-1997;   97US-0063544P.
PR   28-OCT-1997;   97US-0063564P.
PR   29-OCT-1997;   97US-0063734P.
PR   31-OCT-1997;   97US-0063870P.
PR   31-OCT-1997;   97US-0064103P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066120P.
PR   24-NOV-1997;   97US-0066466P.
PR   24-NOV-1997;   97US-0066772P.
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PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
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PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
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PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
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PR 22-APR-1998; 98US-0082704P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
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PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
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PR 28-MAY-1998; 98US-0087098P.
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PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
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PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
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PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
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Query Match 100.0%; Score 2443; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.8e-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 07-JUL-2003 (first entry)
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX

PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
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Query Match 100.0%; Score 2443; DB 6; Length 453;
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KW   tissue typing.
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PN   US2003032112-A1.
XX
PD   13-FEB-2003.
XX
PF   21-JUN-2002; 2002US-00176756.
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DT   05-AUG-2003  (first entry)
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KW   bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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KW   liver; drug screening; transgenic animal; genetic analysis;
KW   antiarthritic; vulnerary; gene therapy.
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
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PD 20-FEB-2003.
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Query Match 100.0%; Score 2443; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.8e-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
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DT 09-AUG-2003 (first entry)

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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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PN US2003040070-A1.
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PD 27-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184627.
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Query Match 100.0%; Score 2443; DB 6; Length 453;
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RESULT 12
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DT 27-JUN-2003 (first entry)
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KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
KW chromosome mapping; gene mapping; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003032113-A1.
XX
PD 13-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176911.
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PR 18-SEP-1997; 97US-0059263P.
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Best Local Similarity 100.0%; Pred. No. 3.8e-188;

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OS   Homo sapiens.
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Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 14
ABR58549
ID ABR58549 standard; protein; 453 AA.
XX
AC ABR58549;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:206.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX

PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72670.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 736-737; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 453 AA;

Query Match 100.0%; Score 2443; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.8e-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
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Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 15
ABR68107
ID ABR68107 standard; protein; 453 AA.
XX
AC ABR68107;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO382, SEQ ID NO:64.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
XX
PD 06-FEB-2003.
XX
PF 18-JUN-2002; 2002US-00174579.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 29-OCT-1997; 97US-0063734P.
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Query Match 100.0%; Score 2443; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.8e-188;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Search completed: May 5, 2004, 15:46:51
Job time : 63 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 5, 2004, 15:44:20 ; Search time 45 Seconds
(without alignments)
3176.217 Million cell updates/sec

Title: US-09-846-512-2
Perfect score: 2443
Sequence: 1 MGENDPPAVEAPFSFRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
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13: sp_vertebrate:*
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17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2225	91.1	453	11	Q812A6	Q812a6 mus musculu
2	1682	68.8	344	4	Q8WY52	Q8wy52 homo sapien
3	882	36.1	492	4	Q96T73	Q96t73 homo sapien
4	877	35.9	490	11	Q7TN04	Q7tn04 mus musculu
5	875.5	35.8	490	11	Q920K3	Q920k3 rattus norv
6	836	34.2	767	13	Q9DGR2	Q9dgr2 xenopus lae
7	813	33.3	326	13	Q7ZZ80	Q7zz80 brachydanio
8	726.5	29.7	581	4	Q9BYE2	Q9bye2 homo sapien
9	720.5	29.5	471	11	Q8CFE0	Q8cfe0 mus musculu
10	718.5	29.4	558	4	Q86YM4	Q86ym4 homo sapien
11	711	29.1	537	4	Q9BYE1	Q9bye1 homo sapien
12	704.5	28.8	445	11	Q8CJ17	Q8cj17 rattus norv
13	700.5	28.7	371	11	Q8CJ16	Q8cj16 rattus norv
14	693.5	28.4	455	11	Q8CDR0	Q8cdr0 mus musculu
15	657.5	26.9	777	11	Q8CAN9	Q8can9 mus musculu
16	656.5	26.9	405	4	Q96E86	Q96e86 homo sapien
17	588.5	24.1	643	6	O97506	O97506 sus scrofa
18	574.5	23.5	638	11	Q8R0P5	Q8r0p5 mus musculu
19	567.5	23.2	572	11	Q8BIK6	Q8bik6 mus musculu
20	565.5	23.1	416	4	Q86T26	Q86t26 homo sapien
21	564.5	23.1	417	11	Q8VHJ4	Q8vhj4 rattus norv
22	563.5	23.1	417	11	Q8BZ10	Q8bz10 mus musculu
23	557.5	22.8	1322	5	Q9NJS5	Q9njs5 anopheles g
24	554.5	22.7	1322	5	Q9NAT0	Q9nat0 anopheles g
25	553	22.6	855	11	Q9JJI7	Q9jji7 rattus norv
26	551.5	22.6	257	11	Q8BZ04	Q8bz04 mus musculu
27	549	22.5	868	5	Q9Y1V3	Q9y1v3 polyandroca
28	547	22.4	845	13	Q9DGR1	Q9dgr1 xenopus lae
29	545.5	22.3	417	11	Q8VDV1	Q8vdv1 mus musculu
30	545.5	22.3	417	11	Q8VHK8	Q8vhk8 mus musculu
31	543.5	22.2	422	4	Q8WVC1	Q8wvc1 homo sapien
32	537.5	22.0	279	11	Q9QZ74	Q9qz74 rattus norv
33	532.5	21.8	336	11	Q80YD8	Q80yd8 mus musculu
34	528.5	21.6	1374	5	Q9VSU0	Q9vsu0 drosophila
35	528.5	21.6	1449	5	Q9U1I2	Q9u1i2 drosophila
36	528.5	21.6	1450	5	Q8IQB8	Q8iqb8 drosophila
37	528.5	21.6	1462	5	Q9U1I3	Q9u1i3 drosophila
38	528.5	21.6	2382	5	Q9BI19	Q9bi19 drosophila
39	528.5	21.6	2409	5	Q960G6	Q960g6 drosophila
40	528.5	21.6	2786	5	Q9VSU2	Q9vsu2 drosophila
41	521.5	21.3	581	5	Q9XZM7	Q9xzm7 strongyloce
42	521	21.3	1111	11	Q80YN4	Q80yn4 rattus norv
43	518.5	21.2	439	11	Q8BHM9	Q8bhm9 mus musculu
44	517.5	21.2	328	11	Q80Z40	Q80z40 rattus norv
45	517.5	21.2	429	13	Q8AVB0	Q8avb0 brachydanio

ALIGNMENTS

RESULT 1
Q812A6
ID Q812A6 PRELIMINARY; PRT; 453 AA.
AC Q812A6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane proteinase tmprss3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Rao N.V., Rao G.N., Hoidal J.R.;
RT "Genomic Organization of Murine Transmembrane Proteinases.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF479687; AAO33581.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50068; LDLRA_2; 1.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.

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DR   PROSITE; PS00135; TRYPSIN_SER; 1.
SQ   SEQUENCE   453 AA;  49505 MW;  1EE7ECD6CB3DD894 CRC64;

  Query Match             91.1%;  Score 2225;  DB 11;  Length 453;
  Best Local Similarity   89.0%;  Pred. No. 6.3e-207;
  Matches  403;  Conservative   25;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              ||||||| |||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 MGENDPPAAEAPFSFRSLFGLDDLKISPVAPDGDAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              |||||||||||||||||| |||||||| |||||||||: ||||||||| || | ||||
Db         61 LALAIGLGIHFDCSGKYRCHSSFKCIELTARCDGVSDCKNAEDEYRCVRVSGQRAALQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              |||:|:|||||||| ||| :|||||||||||||:||| :|| ||: :||||:||| |||
Db        121 TAAAWRTMCSDDWKSHYAKIACAQLGFPSYVSSDHLRVDALEEQFQGDFVSINHLLSDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              |||||||||:|||| |||||||:|:||| | ||| |||||||| |:||||| |||||||
Db        181 VTALHHSVYMREGCTSGHVVTLKCSACGTRTGYSPRIVGGNMSSLTQWPWQVSLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              |||||:|||||:|||||||||| |||||:|||||||:|:| |||||||||:|||||||||
Db        241 LCGGSIITPLWIVTAAHCVYDLYHPKSWTVQVGLVSLMDSPVPSHLVEKIIYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
              |||||||||: ||||:| |||:|||||||||||:||||||||||||||||||||||||||
Db        301 LGNDIALMKLSEPLTFDETIQPICLPNSEENFPDGKLCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLKGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
              |||||||||||||:|||||||||:||||||
Db        421 GIGCAEVNKPGVYTRITSFLDWIHEQLERDLKT 453


RESULT 2
Q8WY52
ID   Q8WY52      PRELIMINARY;      PRT;   344 AA.
AC   Q8WY52;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Potential serine protease TMPRSS3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang Y.C., Chen S.Y., Chang M.S.;
RT   "Cloning and characterization of TMPRSS3, a new member of the serine
RT   protease family.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; AF267741; AAL56664.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   344 AA;  37447 MW;  0A8E8F289972F8BF CRC64;

  Query Match             68.8%;  Score 1682;  DB 4;  Length 344;
  Best Local Similarity   95.2%;  Pred. No. 2e-154;
  Matches  319;  Conservative    3;  Mismatches    9;  Indels    4;  Gaps    1;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
              |||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||
Db        121 TAASWKTMCSDDWKGHYANVACAQLGSPSYVSPDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVC----LPNSEEN 331
              |||||||||||||||||    :|    ||  :|:
Db        301 LGNDIALMKLAGPLTFNGTSGSLCGSAALPLFQED 335


RESULT 3
Q96T73
ID   Q96T73      PRELIMINARY;      PRT;   492 AA.
AC   Q96T73;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Epitheliasin.
GN   TMPRSS2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21223025; PubMed=11322890;
RA   Jacquinet E., Rao N.V., Rao G.V., Wang Z., Albertine K.H.,
RA   Hoidal J.R.;
RT   "Cloning and characterization of the cDNA and gene for human
RT   epitheliasin.";
RL   Eur. J. Biochem. 268:2687-2699(2001).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; AF329454; AAK53559.1; -.
DR   HSSP; P00761; 1AN1.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
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DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   492 AA;  53863 MW;  3ABA755BF276DADF CRC64;

  Query Match           36.1%;  Score 882;  DB 4;  Length 492;
  Best Local Similarity   45.7%;  Pred. No. 1.3e-76;
  Matches  188;  Conservative   54;  Mismatches  149;  Indels   20;  Gaps   10;

Qy         52 IVIGIIALILALAIGLGIHF---DCSGK-YRCRSSFKCIELIARCDGVSDCKDGEDEYRC 107
              : :|    :  ||| ||  |   ||    | ||  ||      ||||| |  |||| ||
Db         89 LTLGTFLVGAALAAGLLWKFMGSKCSNSGIECDSSGTCINPSNWCDGVSHCPGGEDENRC 148

Qy        108 VRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ 164
              ||: | |  :||:::   ||  :| |||  :|   ||  :|:  :: ||  :   |
Db        149 VRLYGPNFILQMYSSQRKSWHPVCQDDWNENYGRAACKDMGYKNNFYSSQGIVDDSGSTS 208

Qy        165 FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNM 222
              |  :   |  ::   |  . :||    : |:|  ||:|:| |||      |  ||||||
Db        209 FMKLNTSAGNV---DIYKKLYHS----DACSSKAVVSLRCIACGVNLNSSRQSRIVGGES 261

Qy        223 SLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLD 279
              :|   |||| ||  |  |:||||:||| ||:|||||   |  |  ||   |::  | :
Db        262 ALPGAWPWQVSLHVQNVHVCGGSIITPEWIVTAAHCVEKPLNNPWHWTAFAGILRQSFMF 321

Qy        280 NPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCW 339
              |  : |||:: |  | |  ||||||||  |||||:::::||||||        ::||
Db        322 YGA-GYQVEKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCW 380

Qy        340 TSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGD 399
              |||||||: |  | ||| | | ||  : || | ||  :|:|:|:|||:| | |||||||
Db        381 ISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGD 440

Qy        400 SGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD 450
              ||||||  :  :| |:| ||:| |||:  :|||| |  | |||: ||  |
Db        441 SGGPLVTSKNNIWWLIGDTSWGSGCAKAYRPGVYGNVMVFTDWIYRQMRAD 491


RESULT 4
Q7TN04
ID   Q7TN04      PRELIMINARY;      PRT;   490 AA.
AC   Q7TN04;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tmprss2 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054348; AAH54348.1; -.
SQ   SEQUENCE   490 AA;  53525 MW;  54650B028417665A CRC64;

  Query Match           35.9%;  Score 877;  DB 11;  Length 490;
  Best Local Similarity   41.0%;  Pred. No. 4.1e-76;
  Matches  193;  Conservative   66;  Mismatches  146;  Indels   66;  Gaps   13;

Qy         28 PVAPDADAVAAQILSLLPLKFFPIIV-----------IGII----------------A 58
              ||||:      :| | :::|  |               :|                 :
Db         31 PVAPNG-------YNLYPAQYYPSPVPQYAPRITTQASTSVIHTHPKSSGALCTSKSKKS 83

Qy         59 LILALAIGLGI--------------HFDCS-GKYRCRSSFKCIELIARCDGVSDCKDGED 103
              | ||||:|  :             :||  :  |  ||   ||     ||||: | :|||
Db         84 LCLALALGTVLTGAAVAAVLLWRFWDSNCSTSEMECGSSGTCISSSLWCDGVAHCPNGED 143

Qy        104 EYRCVRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSS 160
              | ||||: ||: :|||:::   :|  :| |||   |   ||  :|:  :: ||  :   |
Db        144 ENRCVRLYGQSFILQVYSSQRKAWYPVCQDDWSESYGRAACKDMGYKNNFYSSQGIPDQS 203

Qy        161 LEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRR-GYSSRIVG 219
              |  :  ||  ::   |     |:||    : |:|  ||:|:|  || |      |||||
Db        204 GATSFMKLNVSSGNV---DLYKKLYHS----DSCSSRMVVSLRCIECGVRSVKRQSRIVG 256

Qy        220 GNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYD-LYLPKSWTIQVGLV--S 276
              |  :   |||| ||  ||  |:||||:||| ||:|||||| : |  |: ||    |::  |
Db        257 GLNASPGDWPWQVSLHVQGVHVCGGSIITPEWIVTAAHCVEEPLSSPRYWTAFAGILRQS 316

Qy        277 LLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336
              |:     | |||:: |  |  |  ||||||| || ||::::|||||         :
Db        317 LMFY-GSRHQVEKVISHPNYDSKTKNNDIALMKLQTPLAFNDLVKPVCLPNPGMMLDLDQ 375

Qy        337 VCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSC 396
              || |||||| : |  | ||| | ||||    || : :|  :|:|:|:|||:| | ||||
Db        376 ECWISGWGATYEKGKTSDVLNAAMVPLIEPSKCNSKYIYNNLITPAMICAGFLQGSVDSC 435

Qy        397 QGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM 447
              |||||||||  :  :| |:| ||:| |||:  :|||| || | |||::||
Db        436 QGDSGGPLVTLKNGIWWLIGDTSWGSGCAKALRPGVYGNVTVFTDWIYQQM 486


RESULT 5
Q920K3
ID   Q920K3      PRELIMINARY;      PRT;   490 AA.
AC   Q920K3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   TMPRSS2.
GN   TMPRSS2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
```

RA Tsuzuki S.;
RT "TMPRSS2, Rat.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB073550; BAB70683.1; -.
DR HSSP; P00761; 1AN1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS50068; LDLRA_2; 1.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 490 AA; 53518 MW; 2BC691551CAC409A CRC64;

Query Match 35.8%; Score 875.5; DB 11; Length 490;
Best Local Similarity 44.7%; Pred. No. 5.7e-76;
Matches 182; Conservative 62; Mismatches 144; Indels 19; Gaps 10;

```
Qy         52 IVIGIIALILALAIGLGIHF---DC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRC 107
              : :|: : : |:| ||   |    | | :  | ||  ||     ||||: | :|:|| ||
Db         88 LALGLSSPVAAVAAGLLWKFWDSKCSSSEMECGSSGTCISSSLWCDGVAQCPNGKDENRC 147

Qy        108 VRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ 164
              ||: | :  ||:::   :|  :| |||    |   ||  :|:  |: ||  :   |
Db        148 VRLYGTSFTLQVYSSQRKAWYPVCQDDWNESYGRAACKDMGYKNSFYSSQGIPDQSGATS 207

Qy        165 FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRR-GYSSRIVGGNMS 223
              | :  ||  ::   |    |:||    : |:|  ||:|:|  || |      ||||||: :
Db        208 FMKLNVSAGNV---DLYKKLYHS----DSCSSRMVVSLRCIECGVRSVRRQSRIVGGSTA 260

Qy        224 LLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYD-LYLPKSWTIQVGLV--SLLDN 280
              |||| ||  || |:|||:||| ||:|| ||| : |  |: ||  `|::  ||:
Db        261 SPGDWPWQVSLHVQGIHVCGGSIITPEWIVTARHCVEEPLSSPRYWTAFAGILKQSLMFY 320

Qy        281 PAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWT 340
              | |||::  |  |  |  |||||||  || ||::::|||||        : ||
Db        321 -GSRHQVEKVISHPNYDSKTKNNDIALMKLQTPLAFNDVVKPVCLPNPGMMLDLAQECWI 379

Qy        341 SGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDS 400
              |||||| : |  | ||| | ||||    || : :|  :|:|:|:|||:|  | ||||||||
Db        380 SGWGATYEKGKTSDVLNAAMVPLIEPSKCNSKYIYNNLITPAMICAGFLQGSVDSCQGDS 439

Qy        401 GGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM 447
              |||||  :  :| |:| ||:| |||:  :||||  || | |||::||
Db        440 GGPLVTLKNEIWWLIGDTSWGSGCAKAYRPGVYGNVTVFTDWIYQQM 486
```

RESULT 6
Q9DGR2
ID Q9DGR2 PRELIMINARY; PRT; 767 AA.
AC Q9DGR2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Embryonic serine protease-2.
GN XESP-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363741; PubMed=10903452;
RA Yamada K., Takabatake T., Takeshima K.;
RT "Isolation and characterization of three novel serine protease genes
RT from Xenopus laevis.";
RL Gene 252:209-216(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB038497; BAB08217.1; -.
DR HSSP; P00766; 1CHG.
DR MEROPS; S01.049; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00057; ldl_recept_a; 4.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLa; 8.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 767 AA; 86001 MW; E0566A38796DE96E CRC64;

Query Match 34.2%; Score 836; DB 13; Length 767;
Best Local Similarity 45.1%; Pred. No. 7.1e-72;
Matches 175; Conservative 46; Mismatches 131; Indels 36; Gaps 9;

```
Qy         78 RCRSSPKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF--TAASWKTMCSDDWKG 135
              || ||  |:      |||||||  ||||  || :   :  |||:  : ::|  :||| |
Db        394 RCGSSVSCVLSSQWCDGVSDCPYGEDEMSCVSLYPADFQLQVYSTSVSAWLPVCSDYWND 453

Qy        136 HYANVACAQLGP--PSYVSSDNLR--------VSSLEGQFREEFVSIDHLLPDDKVTALH 185
               :  ||   |:   ||   | |                | :| :|          |::
Db        454 DFGRFACQDFGYNGSSYNRYDTLMSPYAPNGYFKLYSGYWRSKF----------YTSVQ 502

Qy        186 HSVYVREGCASGHVVTLQCTACG-HRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGG 244
              :| |     | ||:||:| | :||        ||||||  : |  |||| :||:     ||||
Db        503 YSSY----CYSGNVVSLHCISCGVSNNSLVSRIVGGTFANLGNWPWQVNLQYITGVLCGG 558

Qy        245 SVITPLWIITAAHCVYDLYLPKS-WTIQVGLVSLLDNP----APSHLVEKIVYHSKYKPK 299
              |:|:| ||:|||||||  |   | | :  |    |  |    | :: ||:|: |  ||
Db        559 SIISPKWIVTAAHCVYGSYSSASGWRVFAG---TLTKPSYYNASAYFVERIIVHPGYKSY 615

Qy        300 RLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHA 359
              ||||||||   :||    ||||||||   :  |  | ||||:| :||  |  | :|
Db        616 TYDNDIALMKLRDEITFGYTTQPVCLPNSGMFWEAGTTTWISGWGSTYEGGSVSTYLQYA 675

Qy        360 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 419
              |:||| : :||    || | |: ||:|||||:||||:|||||||||| :    | ||| ||
Db        676 AIPLIDSNVCNQSYVYNGQITSSMICAGYLSGGVDTCQGDSGGPLVNKRNGTWWLVGDTS 735

Qy        420 FGIGCAEVNKPGVYTRVTSFLDWIHEQM 447
              :| |||  ||||||  ||:||:|: ||
Db        736 WGDGCARANKPGVYGNVTTFLEWIYSQM 763
```

RESULT 7
Q7ZZ80
ID Q7ZZ80 PRELIMINARY; PRT; 326 AA.

```
AC   Q7ZZ80;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   SI:dZ69G10.3 (Novel protein similar to human transmembrane protease,
DE   serine 3 (TMPRSS3)) (Fragment).
GN   SI:DZ69G10.3.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Corby N.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL672083; CAD61105.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Transmembrane; Protease.
FT   NON_TER       1       1
SQ   SEQUENCE   326 AA;  35561 MW;  8D6F12214393CDB2 CRC64;

  Query Match             33.3%;  Score 813;  DB 13;  Length 326;
  Best Local Similarity   42.6%;  Pred. No. 3.8e-70;
  Matches  160;  Conservative   47;  Mismatches  101;  Indels   68;  Gaps    4;

Qy         73 CSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWKTMCSDD 132
              ||||: | || :||   | |||| ||:|||||  |||| | ::|||||     |:|:||:
Db          5 CSGKFHCVSSVRCISRNAVCDGVQDCRDGEDELNCVRVSGSHSVLQVFGRGLWRTVCSEG 64

Qy        133 WKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVRE 192
              |    : :|| |||:
Db         65 WDSQLSTLACRQLGY---------------------------------------------- 79

Qy        193 GCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWI 252
                          |   ||||||||:|   | ||| || :|  :|||||:|:  ||
Db         80 ---------------SRSAISSRIVGGNVSKSGQVPWQVSLHYQNQYLCGGSIISESWI 123

Qy        253 ITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAG 312
              :||||||:    |  | :  ||::|  : | :| ||||:||: :: |    ||||:||
Db        124 LTAAHCVFGFAQPVLWDVYAGLINLPLSKAEAHSVEKIIYHANFRSKSFSYDIALIKLTL 183

Qy        313 PLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR 372
              |||||: | |:|||  |:| :|::|  ||||||  | |: |  |: | |||:||| |
Db        184 PLTFNDQIAPICLPNYGESFKNGQMCLISGWGATVDSGETSLSLHVAQVPLLSNKECRKL 243

Qy        373 DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGV 432
                  ::   :| :|  || :|||||||| ||    | |||  |:  | :|||||:
Db        244 G-----LTNWNVCTEFLR-GVGTCQGDSGGPLACQ-GSAWTLVGTGSWDENCGKVNKPGI 296

Qy        433 YTRVTSFLDWIHEQME 448
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              || ::  | || ||||
Db        297 YTSISEALTWIQEQME 312


RESULT 8
Q9BYE2
ID   Q9BYE2      PRELIMINARY;      PRT;   581 AA.
AC   Q9BYE2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Membrane-type mosaic serine protease.
GN   MSPL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=21167393; PubMed=11267681;
RA   Kim D.R., Sharmin S., Inoue M., Kido H.;
RT   "Cloning and expression of novel mosaic serine proteases with and
RT   without a transmembrane domain from human lung.";
RL   Biochim. Biophys. Acta 1518:204-209(2001).
DR   EMBL; AB048796; BAB39741.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.087; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   581 AA;  62689 MW;  4DABE24D7D5BA4A4 CRC64;

  Query Match             29.7%;  Score 726.5;  DB 4;  Length 581;
  Best Local Similarity   38.2%;  Pred. No. 2e-61;
  Matches  158;  Conservative   66;  Mismatches  161;  Indels   29;  Gaps   10;

Qy         44 LPLKFFPIIVIGIIALILALAIGLGIHFDC----SGKYRCRSSFKCIELIARCDGVSDCK 99
              |||          || : |::|| : | | |       :|          | :   ||||| |||
Db        161 LPL-------IGCVLLLIALVVSLIILFQFWQGHTGIRHKEQRESCPKHAVRCDGVVDCK 213

Qy        100 DGEDEYRCVRVGGQNAVLQVFTAAS--WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLR 157
                 ||  |||     ::|:::: :|  |  :|| :|   |:   | |||| |   :  :
Db        214 LKSDELGCVRFDWDKSLLKIYSGSSHQWLPICSSNWNDSYSEKTCRQLGFPESAHRTTEVA 273

Qy        158 VSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRI 217
                       :|  :   :|  :  : :  |:: |  | |   ::|||: ||  |  : ||
Db        274 --------HRDFANSFSILRYN--STIQESLH-RSHCPSQRYISLQCSHCG-LRAMTGRI 321

Qy        218 VGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDL--YLPKSWTIQVGLV 275
              ||| ::  |:|||| || |    |:|||::|   |::|||||  :     : : | :  |
Db        322 VGGALASDSKWPWQVSLHFGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEGWKVYAGTS 381

Qy        276 SLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDG 335
              :|   |  : : | |: :| |  :    |||||:|: ||| :  | | |||   : |
Db        382 NLHQLPEAASIAE-IIINSNYTDEEDDYDIALMRLSKPLTLSAHIHPACLPMHGQTFSLN 440

Qy        336 KVCWTSGWGATEDGGD-ASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVD 394
```

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Db        441 ETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDLHGGRD 500

Qy        395 SCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448

Db        501 SCQGDSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWIYSKME 554


RESULT 9
Q8CFE0
ID   Q8CFE0      PRELIMINARY;      PRT;   471 AA.
AC   Q8CFE0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to mosaic serine protease (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC042878; AAH42878.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00530; SRCR; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Protease.
FT   NON_TER       1      1
SQ   SEQUENCE   471 AA;  52535 MW;  ED58CFE6B7C3BCC4 CRC64;

  Query Match             29.5%;  Score 720.5;  DB 11;  Length 471;
  Best Local Similarity   35.6%;  Pred. No. 5.9e-61;
  Matches  163;  Conservative   74;  Mismatches  176;  Indels   45;  Gaps   11;

Qy         24 LKISPV-------APDADAVAAQILSLLPLKFFP----------IIVIGIIALILALAIG 66

Db         26 VRATPVGAVPIRASPARSAPATRATRESPGLSFPKFSWQETQRQLPLIGCVILLISLVIS 85

Qy         67 LGIHFDCSGKYRCRSSFK-------CIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQV 119

Db         86 LILLFYF---WRGHTGIKYKEPLESCPIHAVRCDGVVDCKMKSDELGCVRFDWDKSLLKV 142

Qy        120 FTAAS--WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLP 177

Db        143 YSGSSGEWLPVCSSSWNDTDSKRTCQQLGFDSAYRTTEVAHRDITSSF----------LL 192

Qy        178 DDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQ 237

Db        193 SEYNTTIQESLY-RSQCPSRRYVSLQCSHCG-LRAMTGRIVGGALTSESKWPWQVSLHFG 250

Qy        238 GYHLCGGSVITPLWIITAAHCVYDL--YLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSK 295

Db        251 TTHICGGTLIDAQWVLTAAHCFFVTREKLLEGWKVYAGTSNLHQLPEAAS-ISQIIINGN 309

Qy        296 YKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGD-ASP 354

Db        310 YTDEQDDYDIALIRLSKPLTLSAHIHPACLPMHGQTFGLNETCWITGFGKTKETDEKTSP 369

Qy        355 VLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKL 414

Db        370 FLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDLRGGRDSCQGDSGGPLVCEQNNRWYL 429

Qy        415 VGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLK 452

Db        430 AGVTSWGTGCGQKNKPGVYTKVTEVLPWIYRKMESEVR 467


RESULT 10
Q86YM4
ID   Q86YM4      PRELIMINARY;      PRT;   558 AA.
AC   Q86YM4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Transmembrane protease serine 6.
GN   TMPRSS6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Park T.J., Park W.J.;
RT   "Homo sapiens transmembrane protease, serine 6 (TMPRSS6) mRNA.";
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY190317; AAO38062.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Protease.
SQ   SEQUENCE   558 AA;  60432 MW;  4AC817FCD70D7017 CRC64;

  Query Match             29.4%;  Score 718.5;  DB 4;  Length 558;
  Best Local Similarity   38.5%;  Pred. No. 1.2e-60;
  Matches  160;  Conservative   64;  Mismatches  159;  Indels   33;  Gaps   11;

Qy         44 LPLKFFPIIVIGIIALILALAIGLGIHFDCSGKY------RCRSSFKCIELIARCDGVSD 97

Db        161 LPL-------IGCVLLLIALVVSLIILFQFWQGYTGIRYKEQRES--CPEHAVRRDGVVD 211

Qy         98 CKDGEDEYRCVRVGGQNAVLQVFTAAS--WKTMCSDDWKGHYANVACAQLGFPSYVSSDN 155

Db        212 CKLKSDELGCVRFDWDKSLLKIYSGSSHQWLPICSSNWNDSYSEKTCQQLGFESAHRTTE 271

Qy        156 LRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSS 215

Db        272 VA--------HRDFANSFSILRYN--STIQESLH-RSECPSQRYISLQCSHCG-LRAMTG 319

Qy        216 RIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDL--YLPKSWTIQVG 273
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```
Db        320 RIVGGALASDSKWPWQVSLHFGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEGWKVYAG 379

Qy        274 LVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFP 333

Db        380 TSNLHQLPEAASIAE-IIINSNYTDEEDDYDIALMRLSKPLTLSAHIHPACLPMHGQTFS 438

Qy        334 DGKVCWTSGWGATEDGGD-ASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGG 392

Db        439 LNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDLRGG 498

Qy        393 VDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448

Db        499 RDSCQGDSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWIYSKME 554
```

RESULT 11
Q9BYE1
ID Q9BYE1 PRELIMINARY; PRT; 537 AA.
AC Q9BYE1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mosaic serine protease.
GN MSPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=21167393; PubMed=11267681;
RA Kim D.R., Sharmin S., Inoue M., Kido H.;
RT "Cloning and expression of novel mosaic serine proteases with and
RT without a transmembrane domain from human lung.";
RL Biochim. Biophys. Acta 1518:204-209(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB048797; BAB39742.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.087; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_a; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00192; LDLa; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 537 AA; 58102 MW; A39FF4E8816DAECF CRC64;

Query Match 29.1%; Score 711; DB 4; Length 537;
Best Local Similarity 39.1%; Pred. No. 5.9e-60;
Matches 146; Conservative 64; Mismatches 145; Indels 18; Gaps 8;

```
Qy         85 CIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS--WKTMCSDDWKGHYANVAC 142

Db        174 CPKHAVRCDGVVDCKLKSDELGCVRFDWDKSLLKIYSGSSHQWLPICSSNWNDSYSEKTC 233

Qy        143 AQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTL 202

Db        234 RQLGFESAHRTTEVA--------HRDFANSFSILRYN--STIQESLH-RSHCPSQRYISL 282

Qy        203 QCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDL 262

Db        283 QCSHCG-LRAMTGRIVGGALASDSKWPWQVSLHFGTTHICGGTLIDAQWVLTAAHCFFVT 341

Qy        263 --YLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMI 320

Db        342 REKVLEGWKVYAGTSNLHQLPEAASIAE-IIINSNYTDEEDDYDIALMRLSKPLTLSAHI 400

Qy        321 QPVCLPNSEENFPDGKVCWTSGWGATEDGGD-ASPVLNHAAVPLISNKICNHRDVYGGII 379

Db        401 HPACLPMHGQTFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYL 460

Qy        380 SPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSF 439

Db        461 TPRMMCAGDLHGGRDSCQGDSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEV 520

Qy        440 LDWIHEQMERDLK 452

Db        521 LPWIYSKMESEVR 533
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RESULT 12
Q8CJ17
ID Q8CJ17 PRELIMINARY; PRT; 445 AA.
AC Q8CJ17;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adrenal mitochondrial protease long variant.
GN AMP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEDH;
RA Omer S., Bicknell A.B., Lowry P.J.;
RT "Identification of a rat adrenal mitochondrial protease.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF537098; AAN06757.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS50287; SRCR_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
SQ SEQUENCE 445 AA; 48440 MW; BE3F56D8372ED988 CRC64;

Query Match 28.8%; Score 704.5; DB 11; Length 445;
Best Local Similarity 35.7%; Pred. No. 1.9e-59;
Matches 148; Conservative 69; Mismatches 169; Indels 29; Gaps 11;

```
Qy         52 IVIGIIALILALAIG---LGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYR-- 106

Db         40 VILGALGLLLAGAGVGSWLLVLYLWPAASPPVSVTLQEEEVTLSCPGVS----SEEKLLPS 95

Qy        107 -----CVRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVS 159

Db         96 LPKAVSFRINGEDLLLEVQVRARPDWLLVCHEGWNPALGMHICQSLGYFRLTQHKAVNLS 155

Qy        160 SLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVG 219
```

```
Db        156 DIKLNRSQEFAQLS-ARPGSLV---EEAWQPSTNCPSGRIVSLKCSECG-ARPLASRIVG 210

Qy        220 GNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK--SWTIQVGLVSL 277

Db        211 GQAVASGRWPWQASVMLGSRHTCGGSVLAPYWVVTAAHCMYSFRLSRLSSWRVHAGLVS- 269

Qy        278 LDNPAPSH---LVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPD 334

Db        270 -HSAVRQHQGTMVEKIIPHPLYSAQNHDYDVALLQLRTPINFSDTVSAVCLPAKEQHFPQ 328

Qy        335 GKVCWTSGWGATEDG-GDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGV 393

Db        329 GSQCWVSGWGHTDPSHTHSSDTLQDTMVPLLSTDLCNSSCMYSGALTHRMLCAGYLDGRA 388

Qy        394 DSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448

Db        389 DACQGDSGGPLVCPSGDTWHLVGVVSWGRGCAEPNRPGVYAKVAEFLDWIHDTVQ 443


RESULT 13
Q8CJ16
ID   Q8CJ16      PRELIMINARY;      PRT;   371 AA.
AC   Q8CJ16;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Adrenal mitochondrial protease short variant.
GN   AMP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEDH;
RA   Omer S., Bicknell A.B., Lowry P.J.;
RT   "Identification of a rat adrenal mitochondrial protease.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF537099; AAN06758.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Protease.
SQ   SEQUENCE   371 AA;  40694 MW;  89A64081D9A1FE26 CRC64;

  Query Match           28.7%;  Score 700.5;  DB 11;  Length 371;
  Best Local Similarity   39.7%;  Pred. No. 3.7e-59;
  Matches  138;  Conservative   55;  Mismatches  140;  Indels   15;  Gaps    8;

Qy        109 RVGGQNAVLQVFTAA--SWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFR 166

Db         29 RINGEDLLLEVQVRARPDWLLVCHEGWNPALGMHICQSLGYFRLTQHKAVNLSDIKLNRS 88

Qy        167 EEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLS 226

Db         89 QEFAQLS-ARPGSLV---EEAWQPSTNCPSGRIVSLKCSECG-ARPLASRIVGGQAVASG 143

Qy        227 QWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK--SWTIQVGLVSLLDNPAPS 284

Db        144 RWPWQASVMLGSRHTCGGSVLAPYWVVTAAHCMYSFRLSRLSSWRVHAGLVS--HSAVRQ 201

Qy        285 H---LVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTS 341

Db        202 HQGTMVEKIIPHPLYSAQNHDYDVALLQLRTPINFSDTVSAVCLPAKEQHFPQGSQCWVS 261

Qy        342 GWGATEDG-GDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDS 400

Db        262 GWGHTDPSHTHSSDTLQDTMVPLLSTDLCNSSCMYSGALTHRMLCAGYLDGRADACQGDS 321

Qy        401 GGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448

Db        322 GGPLVCPSGDTWHLVGVVSWGRGCAEPNRPGVYAKVAEFLDWIHDTVQ 369


RESULT 14
Q8CDR0
ID   Q8CDR0      PRELIMINARY;      PRT;   455 AA.
AC   Q8CDR0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Transmembrane protease.
GN   TMPRSS5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK029714; BAC26577.1; -.
DR   MGD; MGI:1933407; Tmprss5.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
SQ   SEQUENCE   455 AA;  49669 MW;  BE22EB2E7503C74B CRC64;

  Query Match           28.4%;  Score 693.5;  DB 11;  Length 455;
  Best Local Similarity   36.1%;  Pred. No. 2.3e-58;
  Matches  150;  Conservative   63;  Mismatches  173;  Indels   29;  Gaps   11;

Qy         52 IVIGIIALILALAIG---LGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYR-- 106

Db         50 VILGVLGLLLAGAGIASWLLVLYLWPPASPSISGTLQEEEMTLNCPGVS----REEELLPS 105

Qy        107 -----CVRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVS 159

Db        106 LPKTVSFRINGEDLLLQVQVRARPDWLLVCHEGWSPALGMHICKSLGHIRLTQHKAVNLS 165

Qy        160 SLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVG 219

Db        166 DIKLNRSQEFAQLS-ARPGGLV---EESWKPSANCPSGRIVSLKCSECG-ARPLASRIVG 220
```

```
Qy        220 GNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK--SWTIQVGLVSL 277
              |       :||||||:      | || ||: | |::|||||:|   | :  || :  ||||
Db        221 GQAVASGRWPWQASVMLGSRHTCGASVLAPHWVVTAAHCMYSFRLSRLSSWRVHAGLVS- 279

Qy        278 LDNPAPSH---LVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPD 334
                    |   :||||: |  |  :    |:||::|  |: |:: :  ||||  |::||
Db        280 -HGAVRQHQGTMVEKIIPHPLYSAQNHDYDVALLQLRTPINFSDTVGAVCLPAKEQHFPW 338

Qy        335 GKVCWTSGWGATEDG-GDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGV 393
              |  |||| |:      :|    |     |||:|  :||   :| | ::  |||||| |
Db        339 GSQCWVSGWGHTDPSHTHSSDTLQDTMVPLLSTYLCNSSCMYSGALTHRMLCAGYLDGRA 398

Qy        394 DSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              |:||||||||||      | |||  |:| |||| |:|||| :|  ||||||: ::
Db        399 DACQGDSGGPLVCPSGDTWHLVGVVSWGRGCAEPNRPGVYAKVAEFLDWIHDTVQ 453


RESULT 15
Q8CAN9
ID   Q8CAN9      PRELIMINARY;      PRT;   777 AA.
AC   Q8CAN9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Protease (Fragment).
GN   PRSS7 OR A130097D21RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK038356; BAC29973.1; -.
DR   MGD; MGI:1197523; Prss7.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0005044; F:scavenger receptor activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR009003; Cys_Ser_trypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000998; MAM_domain.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00629; MAM; 1.
DR   Pfam; PF00530; SRCR; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00020; MAMDOMAIN.
DR   SMART; SM00042; CUB; 1.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00137; MAM; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01180; CUB; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS00740; MAM_1; 1.
DR   PROSITE; PS50060; MAM_2; 1.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   777 AA;  87314 MW;  A18E2F4ECF06D3A8 CRC64;

  Query Match             26.9%;  Score 657.5;  DB 11;  Length 777;
  Best Local Similarity   37.5%;  Pred. No. 1.5e-54;
  Matches  151;  Conservative   64;  Mismatches  143;  Indels   45;  Gaps   16;

Qy         67 LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
              |||    |   :::|:    || |   ||    |:|| ||  |||         | ::|
Db        391 LGIPEPCQDDEFQCKDG-NCIPLGNLCDSYPHCRDGSDEASCVRFLNGTRSNNGLVQFNI 449

Qy        122 AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
               : |   |:::|    :|  |  ||  |  :: :: :||  |      || ::
Db        450 HSIWHIACAENWTTQISNEVCHLLGLGS--ANSSMPISSTGG---GPFVRVNQ------- 497

Qy        182 TALHHSVYVREG--CASGHVVTLQCT--ACGHRR---GYSSRIVGGNMSLLSQWPWQASL 234
               | : |: :     |:   :: |||   :|| ::     | :|||: :   |||  :|
Db        498 -APNGSLILTPSLQCSQDSLILLQCNHKSCGEKKVTQKVSPKIVGGSDAQAGAWPWVVAL 556

Qy        235 QFQGYH--------LCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-A 282
                ||         ||| |:::  |:::||||||    | |  ||  :||   | | :|
Db        557 ----YHRDRSTDRLLCGASLVSSDWLVSAAHCVYRRNLDPTRWTAVLGLHMQSNLTSPQV 612

Qy        283 PSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSG 342
               :|::|| :  |  :|  ||||:| |    : : : |||:|||   : |  |: |  :|
Db        613 VRRVVDQIVINPHYDRRRKVNDIAMMHLEFKVNYTDYIQPICLPEENQIFIPGRTCSIAG 672

Qy        343 WGATEDGGDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSG 401
              ||  :  |    ||  | ||||||: |  :   |   |: ||:|||| ||:|||||||
Db        673 WGYDKINGSTVDVLKEADVPLISNEKCQQQLPEYN--ITESMICAGYEEGGIDSCQGDSG 730

Qy        402 GPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIH 444
              |||:|||   | ||| ||||: ||  | |||| ||: |::|||
Db        731 GPLMCQENNRWFLVGVTSFGVQCALPNHPGVYVRVSQFIEWIH 773


Search completed: May  5, 2004, 15:48:19
Job time : 47 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 5, 2004, 15:45:40 ; Search time 22 Seconds
(without alignments)
1063.026 Million cell updates/sec

Title: US-09-846-512-2
Perfect score: 2443
Sequence: 1 MGENDPPAVEAPFSFRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2385.5	97.6	454	3	US-09-518-046-2	Sequence 2, Appli
2	2206	90.3	455	3	US-09-261-416-2	Sequence 2, Appli
3	1354	55.4	294	3	US-09-518-046-4	Sequence 4, Appli
4	885	36.2	492	3	US-09-342-749-2	Sequence 2, Appli
5	885	36.2	492	4	US-09-691-840-2	Sequence 2, Appli
6	874	35.8	492	4	US-09-685-166A-895	Sequence 895, App
7	862	35.3	157	3	US-09-518-046-23	Sequence 23, Appl
8	696	28.5	283	3	US-08-807-151-1	Sequence 1, Appli
9	696	28.5	283	4	US-09-478-957-1	Sequence 1, Appli
10	674	27.6	417	4	US-09-820-002-4	Sequence 4, Appli
11	669.5	27.4	798	1	US-08-200-900A-2	Sequence 2, Appli
12	669.5	27.4	798	5	PCT-US94-00616-2	Sequence 2, Appli
13	665.5	27.2	423	4	US-09-656-002-2	Sequence 2, Appli
14	665	27.2	416	2	US-09-000-846-2	Sequence 2, Appli
15	658	26.9	435	3	US-09-008-271A-6	Sequence 6, Appli
16	658	26.9	437	4	US-09-851-588-8	Sequence 8, Appli
17	656.5	26.9	376	4	US-09-820-002-2	Sequence 2, Appli
18	656.5	26.9	406	4	US-09-851-588-6	Sequence 6, Appli
19	585.5	24.0	256	2	US-09-027-337-3	Sequence 3, Appli
20	585.5	24.0	256	4	US-09-644-600-3	Sequence 3, Appli
21	585.5	24.0	256	4	US-09-654-600A-3	Sequence 3, Appli
22	580.5	23.8	255	3	US-08-944-483-67	Sequence 67, Appl
23	579.5	23.7	638	2	US-08-681-151-3	Sequence 3, Appli
24	571	23.4	418	1	US-08-508-448C-25	Sequence 25, Appl
25	571	23.4	418	4	US-09-370-838-82	Sequence 82, Appl
26	571	23.4	418	4	US-09-370-838-83	Sequence 83, Appl
27	569	23.3	418	4	US-09-370-838-62	Sequence 62, Appl
28	543.5	22.2	855	2	US-09-027-337-2	Sequence 2, Appli
29	543.5	22.2	855	4	US-09-644-600-2	Sequence 2, Appli
30	543.5	22.2	855	4	US-09-654-600A-2	Sequence 2, Appli
31	539.5	22.1	232	1	US-08-508-448C-19	Sequence 19, Appl
32	539	22.1	248	3	US-08-944-483-63	Sequence 63, Appl
33	536.5	22.0	235	3	US-08-807-151-3	Sequence 3, Appli
34	536.5	22.0	235	4	US-09-478-957-3	Sequence 3, Appli
35	532.5	21.8	285	4	US-09-023-942A-26	Sequence 26, Appl
36	526	21.5	338	4	US-08-991-761A-10	Sequence 10, Appl
37	525.5	21.5	235	3	US-08-944-483-65	Sequence 65, Appl
38	523.5	21.4	790	4	US-08-991-761A-13	Sequence 13, Appl
39	523	21.4	98	3	US-09-518-046-17	Sequence 17, Appl
40	522.5	21.4	407	4	US-09-734-675-4	Sequence 4, Appli
41	519	21.2	405	4	US-09-734-675-2	Sequence 2, Appli
42	507	20.8	314	3	US-09-008-271A-3	Sequence 3, Appli
43	507	20.8	314	4	US-09-907-794A-257	Sequence 257, App
44	507	20.8	314	4	US-09-905-125A-257	Sequence 257, App
45	507	20.8	314	4	US-09-902-775A-257	Sequence 257, App

ALIGNMENTS

RESULT 1
US-09-518-046-2
; Sequence 2, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete amino acid sequence of TADG-12
; OTHER INFORMATION: protein
US-09-518-046-2

Query Match 97.6%; Score 2385.5; DB 3; Length 454;
Best Local Similarity 97.8%; Pred. No. 1.3e-223;
Matches 444; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

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Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFF-PIIVIGIIAL 59
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Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPFEVFSQSSSLGIIAL 60

Qy         60 ILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQV 119
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Db         61 ILALAIGLGIHFDCSGKYRCRSSFKCIELITRCDGVSDCKDGEDEYRCVRVGGQNAVLQV 120

Qy        120 FTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDD 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDD 180

Qy        180 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY 239
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Db        181 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY 240

Qy        240 HLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPK 299
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Db        241 HLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPK 300

Qy        300 RLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHA 359
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Db        301 RLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHA 360

Qy        360 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 419
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Db        361 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 420

Qy        420 FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Db        421 FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 454


RESULT 2
US-09-261-416-2
; Sequence 2, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
;  APPLICANT: O'Brien, Timothy J.
;  APPLICANT: Underwood, Lowell J.
;  TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
;  TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
;  FILE REFERENCE: D6192
;  CURRENT APPLICATION NUMBER: US/09/261,416A
;  CURRENT FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of TADG-12 encoded by nucleotides
;   OTHER INFORMATION: 144 to 1511 of Sequence 1
; Patent No. 6291663
US-09-261-416-2

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  Best Local Similarity   91.7%;  Pred. No. 3.7e-206;
  Matches  421;  Conservative    5;  Mismatches   23;  Indels   10;  Gaps    3;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFF-PIIVIGIIAL 59
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Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPFEVFSQSSSLGIIAL 60

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Db         61 ILALAIGLGIHFDCSGKYRCRSSFKCIELITRCDGVSDCKDGEDEYRCVRVGGQNAVLQV 120

Qy        120 FTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDD 179
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Qy        180 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY 239
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Db        181 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY 240

Qy        240 HLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPK 299
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Db        241 HLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPK 300

Qy        300 RLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHA 359
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Db        417 VGATSFGIGCADVNKPGVYTRVTSFLDWIHEQMERDLKT 455


RESULT 3
US-09-518-046-4
; Sequence 4, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
;  APPLICANT: O'Brien, Timothy J.
;  APPLICANT: Underwood, Lowell J.
;  TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
;  TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
;  FILE REFERENCE: D6192CIP
;  CURRENT APPLICATION NUMBER: US/09/518,046
;  CURRENT FILING DATE: 2000-03-02
;  EARLIER APPLICATION NUMBER: 09/261,416
;  EARLIER FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
;   LENGTH: 294
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: complete amino acid sequence of TADG-12
;   OTHER INFORMATION: variant protein
US-09-518-046-4

  Query Match             55.4%;  Score 1354;  DB 3;  Length 294;
  Best Local Similarity   88.1%;  Pred. No. 1.6e-123;
  Matches  258;  Conservative    7;  Mismatches   20;  Indels    8;  Gaps    2;

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Qy        180 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY 239
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Db        181 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY 240

Qy        240 HLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSL-------LDNPAPSH 285
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Db        241 HLCGGSVITPLWIITAAHCVYEIVAPRERADRRGRKLLCWRKPTKMKGPRPSH 293


RESULT 4
US-09-342-749-2
; Sequence 2, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.C.
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: Teng, DAvid H.-F.
;  APPLICANT: Myriad Genetics, Inc.
;  TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
;  FILE REFERENCE: 2318-202
;  CURRENT APPLICATION NUMBER: US/09/342,749
;  CURRENT FILING DATE: 1999-06-29
;  EARLIER APPLICATION NUMBER: US 60/091,044
;  EARLIER FILING DATE: 1998-06-29
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 492
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-342-749-2

  Query Match             36.2%;  Score 885;  DB 3;  Length 492;
  Best Local Similarity   46.0%;  Pred. No. 1.4e-77;
  Matches  189;  Conservative   53;  Mismatches  149;  Indels   20;  Gaps   10;
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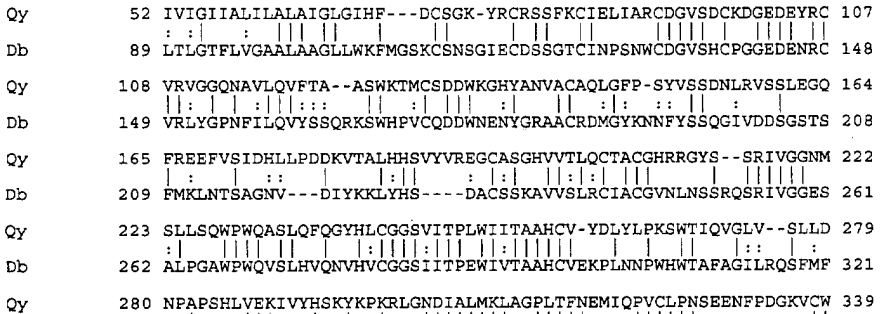
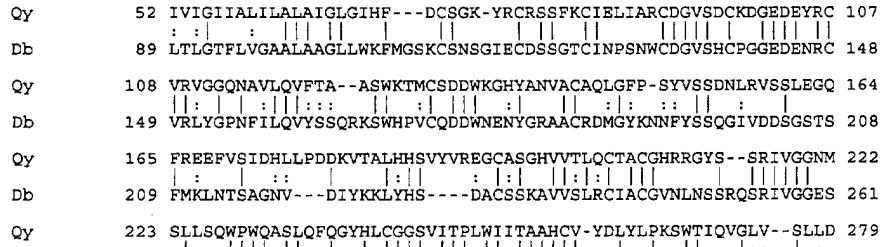
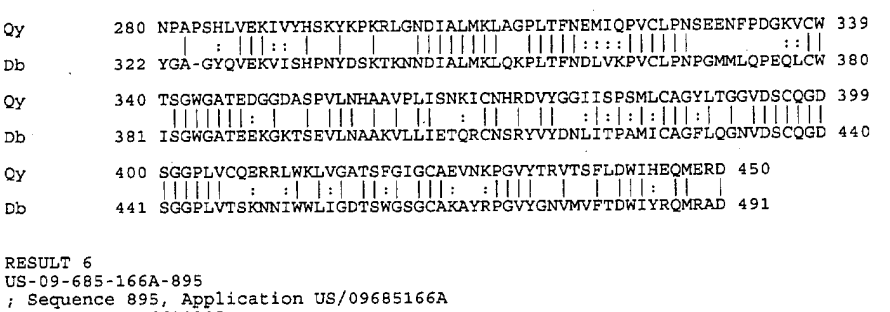


RESULT 5
US-09-691-840-2
; Sequence 2, Application US/09691840
; Patent No. 6444419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, DAvid H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-691-840-2

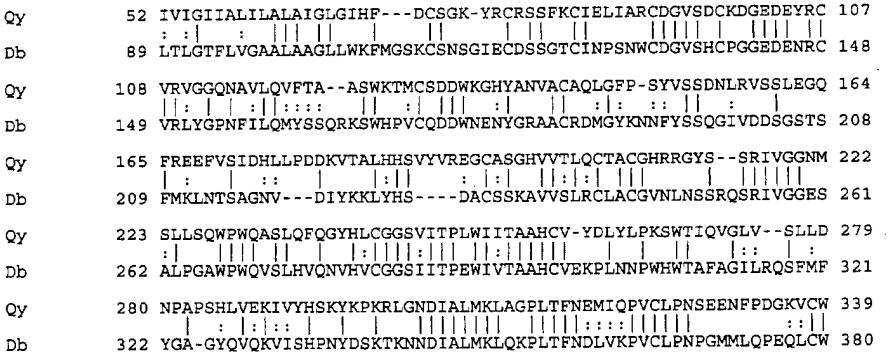
Query Match 36.2%; Score 885; DB 4; Length 492;
Best Local Similarity 46.0%; Pred. No. 1.4e-77;
Matches 189; Conservative 53; Mismatches 149; Indels 20; Gaps 10;





RESULT 6
US-09-685-166A-895
; Sequence 895, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 895
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-895

Query Match 35.8%; Score 874; DB 4; Length 492;
Best Local Similarity 45.5%; Pred. No. 1.7e-76;
Matches 186; Conservative 55; Mismatches 148; Indels 20; Gaps 10;



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Db        381 ISGWGATEEKGKTSEVLNAAKVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGD 440

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RESULT 7
US-09-518-046-23
; Sequence 23, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
;  APPLICANT: O'Brien, Timothy J.
;  APPLICANT: Underwood, Lowell J.
;  TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
;  TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
;  FILE REFERENCE: D6192CIP
;  CURRENT APPLICATION NUMBER: US/09/518,046
;  CURRENT FILING DATE: 2000-03-02
;  EARLIER APPLICATION NUMBER: 09/261,416
;  EARLIER FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 23
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   OTHER INFORMATION: protease domain of TADG-12 (TADG12)
US-09-518-046-23

  Query Match           35.3%;  Score 862;  DB 3;  Length 157;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-76;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        310 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKIC 369
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Db         61 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKIC 120

Qy        370 NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVC 406
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Db        121 NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVC 157


RESULT 8
US-08-807-151-1
; Sequence 1, Application US/08807151
; Patent No. 6043033
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Lal, Preeti
;    TITLE OF INVENTION:  NOVEL HUMAN PROSTATE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEASE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/807,151
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0227 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  283 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  SCORN0T01
;      CLONE:  556016
US-08-807-151-1

  Query Match           28.5%;  Score 696;  DB 3;  Length 283;
  Best Local Similarity  50.4%;  Pred. No. 1.6e-59;
  Matches  137;  Conservative   37;  Mismatches   92;  Indels    6;  Gaps    4;

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              |   |||||||  |||||:::||||||        ::|| |||||||: |  | |||
Db        131 KTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEEKGKTSEVLNA 190

Qy        359 AAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGAT 418
              | | ||  : || | ||  :|:|:|:|||:| | ||||||||||| ||  :  :| |:| |
Db        191 AKVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGXLVTSKNNIWWLIGDT 250

Qy        419 SFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD 450
              |:| |||:  :|||  |  | |||: ||  |
Db        251 SWGSGCAKAYRPGVYGNVMVFTDWIYRQMRAD 282


RESULT 9
US-09-478-957-1
; Sequence 1, Application US/09478957
; Patent No. 6350448
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Lal, Preeti
;    TITLE OF INVENTION:  NOVEL HUMAN PROSTATE-ASSOCIATED
;    TITLE OF INVENTION:  PROTEASE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/09/478,957
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/807,151
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0227 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  283 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  SCORN0T01
;      CLONE:  556016
US-09-478-957-1
```

Query Match 28.5%; Score 696; DB 4; Length 283;
Best Local Similarity 50.4%; Pred. No. 1.6e-59;
Matches 137; Conservative 37; Mismatches 92; Indels 6; Gaps 4;

```
Qy        184 LHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNMSLLSQWPWQASLQFQGYHL 241
              ::  :|  : |:|  ||:|:| |||     |  |||||  :|   |||| ||  |  |:
Db         12 IYKKLYHSDACSSKAVVSLRCIACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNVHV 71

Qy        242 CGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLDNPAPSHLVEKIVYHSKYKP 298
              ||||:||| ||:|||||    |  |  ||    |::  | :   |  : |||:: |  |
Db         72 CGGSIITPEWIVTAAHCVEKPLNNPWHWTAFAGILRQSFMFYGA-GYQVEKVISHPNYDS 130

Qy        299 KRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNH 358
              |   |||||||  |||||:::|||||        ::|| |||||||: |  | |||
Db        131 KTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEEKGKTSEVLNA 190

Qy        359 AAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGAT 418
              | | ||  : || | ||  :|:|:|:|||:| | |||||||||| ||  :  :| |:| |
Db        191 AKVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGXLVTSKNNIWWLIGDT 250

Qy        419 SFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD 450
              |:| |||:  :|||| |  | |||: ||  |
Db        251 SWGSGCAKAYRPGVYGNVMVFTDWIYRQMRAD 282
```

```
RESULT 10
US-09-820-002-4
; Sequence 4, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
;  APPLICANT: Gan, Weiniu
;  APPLICANT:  Ye, Jane
;  APPLICANT:  DiFrancesco, Valentina
;  APPLICANT:  Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001194
;  CURRENT APPLICATION NUMBER: US/09/820,002
;  CURRENT FILING DATE:  2001-03-29
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-820-002-4
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Query Match 27.6%; Score 674; DB 4; Length 417;
Best Local Similarity 35.8%; Pred. No. 3.8e-57;
Matches 149; Conservative 62; Mismatches 143; Indels 62; Gaps 11;

```
Qy         59 LILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQ 118
              |:|  |||               :|:  : :: | |        ::    |:|   :| |
Db         26 LLLLTAIG------------AASWAIVAVLLRSD--------QEPLYPVQVSSADARLM 64

Qy        119 VF--TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLL 176
              ||  |  :|: :||        | ::| ::||   ::   | | :         |  :|
Db         65 VFDKTEGTWRLLCSSRSNARVAGLSCEEMGFLRALTHSELDVRTAGANGTSGFFCVDE-- 122

Qy        177 PDDKVTALHHSVYVRE-----GCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQ 231
                |:  : |       |  |  :   |  || |:    |||||  : | :||||
Db        123 -----GRLPHTQRLLEVISPSDCPRGRFLAAICQDCGRRKLPVDRIVGGRDTSLGRWPWQ 177

Qy        232 ASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK------SWTIQVGLVSLLDNPAPSH 285
              ||:: | ||||||:::  |::|||||       |:       | :  | |:     :|
Db        178 VSLRYDGAHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRVFAGAVA---QASPHG 229

Qy        286 L---VEKIVYHSKYKPKR------LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336
              |   |: :|||  | | |       |||||: |: ||   | ||||||| : :   |||
Db        230 LQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQALVDGK 289

Qy        337 VCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSC 396
              :|  :||| |:  | : ||  | ||:||| :||  | ||  |  | | ||||  ||:|:|
Db        290 ICTVTGWGNTQYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDAC 349

Qy        397 QGDSGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              ||||||| ||:       |:| |  |:| |||   ||||||:|: | :|| : ::
Db        350 QGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWIFQAIK 405
```

```
RESULT 11
US-08-200-900A-2
; Sequence 2, Application US/08200900A
; Patent No. 5665566
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION:  CLONING OF ENTEROKINASE AND METHOD OF USE
;   NUMBER OF SEQUENCES:  38
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genetics Institute, Inc. - Legal Affairs
;     STREET:  87 CambridgePark Drive
;     CITY:  Cambridge
;     STATE:  MA
;     COUNTRY:  USA
;     ZIP:  02140
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/200,900A
;     FILING DATE:  23-FEB-1994
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Meinert, Maureen C.
;     REGISTRATION NUMBER:  31,544
;     REFERENCE/DOCKET NUMBER:  GI 5201-FWC
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (617) 876-1170 X8574
;     TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  798 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-200-900A-2
```

Query Match 27.4%; Score 669.5; DB 1; Length 798;

Best Local Similarity 37.0%; Pred. No. 2.6e-56;
Matches 146; Conservative 70; Mismatches 146; Indels 33; Gaps 14;

```
Qy         66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
              ||||    |    ::|:   :|| |:  |||    |||| ||  |||:       : ::|
Db        415 GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 473

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
                : |   |:::|    ::  |  ||  :   : ::   |  |      :|:::
Db        474 IQSIWHVACAENWTTQISDDVCQLLGLGT--GNSSVPTFSTGG---GPYVNLN------- 521

Qy        181 VTALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQAS 233
               || : |: :   : |    :: |||   :|| :   :  | :||||: |    |||  :
Db        522 -TAPNGSLILTPSQQCLEDSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVA 580

Qy        234 LQFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEK 289
               | |     :|| |:::  |:::|||||    : |  |   :||   | | :|   : |:::
Db        581 LYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQ 640

Qy        290 IVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG 349
               || :  |  :|  ||||:| |   : : : |||:|||   : || |::|  :||||
Db        641 IVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQ 700

Qy        350 GDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQE 408
               |  : ||  | |||:||: |  :   |   |: :|:|||| ||||||||||||||:|||
Db        701 GSTADVLQEADVPLLSNEKCQQQMPEYN--ITENMVCAGYEAGGVDSCQGDSGGPLMCQE 758

Qy        409 RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
                | | | ||||  ||  |:|||| ||  | :||
Db        759 NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWI 793
```

RESULT 12
PCT-US94-00616-2
; Sequence 2, Application PC/TUS9400616
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 33
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00616
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-00616-2

Query Match 27.4%; Score 669.5; DB 5; Length 798;
Best Local Similarity 37.0%; Pred. No. 2.6e-56;
Matches 146; Conservative 70; Mismatches 146; Indels 33; Gaps 14;

```
Qy         66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
              ||||    |    ::|:   :|| |:  |||    |||| ||  |||:       : ::|
Db        415 GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 473

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
                : |   |:::|    ::  |  ||  :   : ::   |  |      :|:::
Db        474 IQSIWHVACAENWTTQISDDVCQLLGLGT--GNSSVPTFSTGG---GPYVNLN------- 521

Qy        181 VTALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQAS 233
               || : |: :   : |    :: |||   :|| :   :  | :||||: |    |||  :
Db        522 -TAPNGSLILTPSQQCLEDSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVA 580

Qy        234 LQFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEK 289
               | |     :|| |:::  |:::|||||    : |  |   :||   | | :|   : |:::
Db        581 LYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQ 640

Qy        290 IVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG 349
               || :  |  :|  ||||:| |   : : : |||:|||   : || |::|  :||||
Db        641 IVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQ 700

Qy        350 GDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQE 408
               |  : ||  | |||:||: |  :   |   |: :|:|||| ||||||||||||||:|||
Db        701 GSTADVLQEADVPLLSNEKCQQQMPEYN--ITENMVCAGYEAGGVDSCQGDSGGPLMCQE 758

Qy        409 RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
                | | | ||||  ||  |:|||| ||  | :||
Db        759 NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWI 793
```

RESULT 13
US-09-656-002-2
; Sequence 2, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND M
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/656,002
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-656-002-2

Query Match 27.2%; Score 665.5; DB 4; Length 423;
Best Local Similarity 35.4%; Pred. No. 2.6e-56;
Matches 160; Conservative 72; Mismatches 157; Indels 63; Gaps 16;

```
Qy         26 ISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALIL---ALAIGLGIHFDCSGKYRCRSS 82
              :|| |          |::|| |    |||: : | :||       |  :||
Db          9 VSPWRPSESVGIPLIIALLSLASI-IIVVVLIKVILDKYYFLCGQPLHF----------- 56

Qy         83 FKCIELIARCDGVSDCKDGEDEYRC----------VRVGGQNAVLQVFTAA--SWKTMC 129
                 |    |||  ||  ||||  |             ||:    : |||  :|  : | :
Db         57 ---IPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSAC 113

Qy        130 SDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVY 189
               |::    |  || |:|: |             :  ||   :  |  |   ::|     :
Db        114 FDNFTEALAETACRQMGYSS------------KPTFRAVEIGPDQDLDVVEITENSQELR 161

Qy        190 VREG---CASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSV 246
               :|      | || :|:|  | ||| :   : |:|||  : :  |||| |:|:   |:|||||:
Db        162 MRNSSGPCLSGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSI 220

Qy        247 ITPLWIITAAHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYKPKR 300
               : | |::|||||      |::   :| :: |    |       ||  | ||:   ::  | ||
Db        221 LDPHWVLTAAHCFRKHTDVF---NWKVRAGSDKL--GSFPSLAVAKIIIIEFNPMY-PK- 273

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGAT-EDGGDASPVLNHA 359
               ||||||||  ||||:  ::|:|||  :|         |  ||| | ::||  | :|  |
Db        274 -DNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQA 332

Qy        360 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 419
```

```
Db        333 SVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ-WHVVGIVS 391

Qy        420 FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDL 451
Db        392 WGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 423


RESULT 14
US-09-000-846-2
; Sequence 2, Application US/09000846
; Patent No. 5981830
;  GENERAL INFORMATION:
;    APPLICANT:  WU, QINGYU
;    APPLICANT:  SADLER, JASPER
;    TITLE OF INVENTION:  KNOCKOUT MICE AND THEIR PROGENY WITH
;    TITLE OF INVENTION:  DISRUPTED SERINE PROTEASE GENES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/000,846
;      FILING DATE:  30-DEC-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/866,058
;      FILING DATE:  30-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LEBOVITZ, RICHARD M.
;      REGISTRATION NUMBER:  37,067
;      REFERENCE/DOCKET NUMBER:  BERLX 65P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  416 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-000-846-2

  Query Match           27.2%;  Score 665;  DB 2;  Length 416;
  Best Local Similarity   38.1%;  Pred. No. 2.9e-56;
  Matches  143;  Conservative   54;  Mismatches  136;  Indels   42;  Gaps    9;

Qy        100 DGEDEYRCVRVGGQNAVLQVF--TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLR 157
Db         46 DQEPLYQ-VQLSPGDSRLAVFDKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAHSELD 104

Qy        158 VSSLEGQFREEFVSID--------HLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGH 209
Db        105 VRTAGANGTSGFFCVDEGGLRLAQRLL--DVISVC--------DCPRGRFLTATCQDCGR 154

Qy        210 RRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK--- 266
Db        155 RKLPVDRIVGGQDSSLGRWPWQVSLRYDGTHLCGGSLLSGDWVLTAAHC-----FPERNR 209

Qy        267 ---SWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR------LGNDIALMKLAGPLTFN 317
Db        210 VLSRWRVFAGAVARTSPHAVQLGVQAVIYHGGYLPFRDPTIDENSNDIALVHLSSSLPLT 269

Qy        318 EMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGG 377
```

```
Db        270 EYIQPVCLPAAGQALVDGKVCTVTGWGNTQFYGQQAMVLQEARVPIISNEVCNSPDFYGN 329

Qy        378 IISPSMLCAGYLTGGVDSCQGDSGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVY 433
Db        330 QIKPKMFCAGYPEGGIDACQGDSGGPFVCEDSISGTSRWRLCGIVSWGTGCALARKPGVY 389

Qy        434 TRVTSFLDWIHEQME 448
Db        390 TKVTDFREWIFKAIK 404


RESULT 15
US-09-008-271A-6
; Sequence 6, Application US/09008271A
; Patent No. 6203979
;  GENERAL INFORMATION:
;       APPLICANT: Bandman, Olga
;                  Hillman, Jennifer L.
;                  Yue, Henry
;                  Guegler, Karl J.
;                  Corley, Neil C.
;                  Tang, Tom Y.
;                  Shah, Purvi
;       TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
;       NUMBER OF SEQUENCES: 24
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Incyte Pharmaceuticals, Inc.
;            STREET: 3174 Porter Dr.
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/008,271A
;            FILING DATE: 16-Jan-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mohan-Peterson, Sheela
;            REGISTRATION NUMBER: 41,201
;            REFERENCE/DOCKET NUMBER: PF-0458 US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-855-0555
;            TELEFAX: 650-845-4166
;  INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 435 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;            LIBRARY: COLNNOT13
;            CLONE: 1337018
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-008-271A-6

  Query Match           26.9%;  Score 658;  DB 3;  Length 435;
  Best Local Similarity   35.7%;  Pred. No. 1.5e-55;
  Matches  158;  Conservative   74;  Mismatches  147;  Indels   64;  Gaps   18;

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Qy        256 AHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYKPKRLGNDIALMK 309
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Qy        369 CNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVN 428
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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-846-512-2
Perfect score: 2443
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2443	100.0	453	9	US-09-978-697-69	Sequence 69, Appl
3	2443	100.0	453	9	US-09-978-192A-69	Sequence 69, Appl
4	2443	100.0	453	9	US-09-999-832A-69	Sequence 69, Appl
5	2443	100.0	453	10	US-09-978-189-69	Sequence 69, Appl
6	2443	100.0	453	10	US-09-978-608A-69	Sequence 69, Appl
7	2443	100.0	453	10	US-09-978-585A-69	Sequence 69, Appl
8	2443	100.0	453	10	US-09-978-191A-69	Sequence 69, Appl
9	2443	100.0	453	10	US-09-978-403A-69	Sequence 69, Appl
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ALIGNMENTS

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; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 2443; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
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;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C9
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
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; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
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; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085579

; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
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Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
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Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 5
US-09-978-189-69
; Sequence 69, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
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Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
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Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 6
US-09-978-608A-69
; Sequence 69, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

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;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 69
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-608A-69

  Query Match            100.0%;  Score 2443;  DB 10;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-225;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
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Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
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Db        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300

Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453


RESULT 7
US-09-978-585A-69
; Sequence 69, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 69
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-585A-69

  Query Match            100.0%;  Score 2443;  DB 10;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-225;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
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Db          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
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Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Db        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420

Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 8
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; Sequence 69, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60
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Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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Db         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Qy        241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR 300
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RESULT 9
US-09-978-403A-69
; Sequence 69, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 2443; DB 10; Length 453;
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Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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RESULT 10
US-09-978-564A-69
; Sequence 69, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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RESULT 11
US-09-999-833A-69
; Sequence 69, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120
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Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 12
US-09-981-915A-69
; Sequence 69, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
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Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Db        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240

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Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Db        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360

Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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RESULT 13
US-09-978-824-69
; Sequence 69, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2443; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-225;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180

Qy        181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240
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Qy        301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAA 360
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Qy        361 VPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSF 420
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Qy        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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RESULT 14
US-09-918-585A-69
; Sequence 69, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
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  Best Local Similarity  100.0%;  Pred. No. 2.3e-225;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C21
;  CURRENT APPLICATION NUMBER: US/09/978,423A
;  CURRENT FILING DATE:  2002-05-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0%; Score 2443; DB 10; Length 453;
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Db        421 GIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 453
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Search completed: May 5, 2004, 15:54:14
Job time : 49 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 5, 2004, 15:44:50 ; Search time 20 Seconds
(without alignments)
2178.738 Million cell updates/sec

Title: US-09-846-512-2
Perfect score: 2443
Sequence: 1 MGENDPPAVEAPFSFRSLFG.....TRVTSFLDWIHEQMERDLKT 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	674	27.6	417	1	S00845	hepsin (EC 3.4.21.
2	669.5	27.4	1035	1	A43090	enteropeptidase (E
3	664.5	27.2	1019	1	A56318	enteropeptidase (E
4	663.5	27.2	1034	1	A53663	enteropeptidase (E
5	654.5	26.8	416	1	S33777	hepsin (EC 3.4.21.
6	579.5	23.7	638	1	KQRTPL	plasma kallikrein
7	570.5	23.4	638	1	KQMSPL	plasma kallikrein
8	553	22.6	855	2	JC7731	membrane-bound arg
9	549.5	22.5	638	1	KQHUP	plasma kallikrein
10	527	21.6	761	2	JC5759	brain-specific ser
11	526	21.5	455	2	A61545	plasmin (EC 3.4.21
12	523.5	21.4	790	1	PLPG	plasmin (EC 3.4.21
13	506.5	20.7	1113	2	JE0315	low-density lipopr
14	504	20.6	273	2	A47246	tryptase (EC 3.4.2
15	504	20.6	625	1	KFHU1	coagulation factor
16	504	20.6	812	1	PLMS	plasmin (EC 3.4.21
17	502	20.5	275	2	A32410	tryptase (EC 3.4.2
18	502	20.5	810	1	PLHU	plasmin (EC 3.4.21
19	500.5	20.5	460	2	B61545	plasmin (EC 3.4.21
20	499	20.4	810	2	I46260	plasmin (EC 3.4.21
21	495.5	20.3	437	2	S18407	acrosin (EC 3.4.21
22	495	20.3	270	2	S56160	mast cell tryptase
23	495	20.3	810	2	B30848	plasmin (EC 3.4.21
24	495	20.3	812	1	PLBO	plasmin (EC 3.4.21
25	493	20.2	276	2	A38654	mast cell proteina
26	493	20.2	436	2	JX0172	acrosin (EC 3.4.21
27	492	20.1	418	2	A37344	acrosin (EC 3.4.21
28	490	20.1	274	2	JC4171	tryptase (EC 3.4.2
29	489	20.0	421	1	S11674	acrosin (EC 3.4.21
30	488	20.0	431	2	S47538	acrosin (EC 3.4.21
31	482	19.7	275	2	A35863	tryptase (EC 3.4.2
32	481	19.7	275	2	B35863	tryptase (EC 3.4.2
33	478	19.6	343	1	A57014	prostasin (EC 3.4.
34	476.5	19.5	264	2	I38136	chymotrypsin-like
35	476	19.5	275	2	C35863	tryptase (EC 3.4.2
36	472	19.3	421	2	S29599	acrosin (EC 3.4.21
37	469.5	19.2	1524	2	T30337	polyprotein - Afri
38	467	19.1	263	1	KYRTB	chymotrypsin (EC 3
39	466	19.1	263	2	A31299	chymotrypsin (EC 3
40	465	19.0	263	2	A21195	chymotrypsin (EC 3
41	464.5	19.0	274	2	A45754	tryptase (EC 3.4.2
42	463	19.0	277	2	S35340	trypsin (EC 3.4.21
43	463	19.0	415	1	A34170	acrosin (EC 3.4.21
44	462	18.9	263	2	S47537	chymotrypsin (EC 3
45	461	18.9	275	2	S40005	trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1
S00845
hepsin (EC 3.4.21.-) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: S00845
R;Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
Biochemistry 27, 1067-1074, 1988
A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom
A;Reference number: S00845; MUID:88209431; PMID:2835076
A;Accession: S00845
A;Molecule type: mRNA
A;Residues: 1-417 <LEY>
A;Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064
C;Genetics:
A;Gene: GDB:HPN; TMPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
A;Map position: 19q11-19q13.2
C;Superfamily: hepsin; trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: transmembrane #status predicted <TMN>
F;163-400/Domain: trypsin homology <TRY>
F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F;203,257,353/Active site: His, Asp, Ser #status predicted

Query Match 27.6%; Score 674; DB 1; Length 417;
Best Local Similarity 35.8%; Pred. No. 1.7e-46;
Matches 149; Conservative 62; Mismatches 143; Indels 62; Gaps 11;

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Qy         59 LILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQ 118
              |:|  |||                 :|:  : :: | |         ::    |:|   :| |
Db         26 LLLLTAIG-------------AASWAIVAVLLRSD--------QEPLYPVQVSSADARLM 64

Qy        119 VF--TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLL 176
              ||  |  :|: :||         | ::| ::||    ::   | | :          |  :|
Db         65 VFDKTEGTWRLLCSSRSNARVAGLSCEEMGFLRALTHSELDVRTAGANGTSGFFCVDE-- 122

Qy        177 PDDKVTALHHSVYVRE-----GCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQ 231
                | |:  : |       |  |  :    |  || |:     |||||  : | :||||
Db        123 -----GRLPHTQRLLEVISVCDCPRGRFLAAICQDCGRRKLPVDRIVGGRDTSLGRWPWQ 177

Qy        232 ASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK------SWTIQVGLVSLLDNPAPSH 285
               ||:: | ||||||:::  |::|||||       |:        | :  | |:     :|
Db        178 VSLRYDGAHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRVFAGAVA---QASPHG 229

Qy        286 L---VEKIVYHSKYKPKR------LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336
              |   |: :|||  | | |         |||||: |: ||   | |||||||  : :   |||
Db        230 LQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQALVDGK 289

Qy        337 VCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSC 396
              :|  :||| |:  |  : ||  | ||:||| :||  | ||  | | | |||| ||:|:|
Db        290 ICTVTGWGNTQYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDAC 349
```

```
Qy        397 QGDSGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448
              ||||||| ||::       |:| |  |:| |||   ||||||:|: | :|| : ::
Db        350 QGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWIFQAIK 405


RESULT 2
A43090
enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine
N;Alternate names: enterokinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Apr-2003
C;Accession: A43090; A48874; A61436
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
A;Reference number: A43090; MUID:94329561; PMID:8052624
A;Accession: A43090
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1035 <KIT>
A;Cross-references: GB:U09859; NID:g746410; PIDN:AAB40026.1; PID:g746411
A;Experimental source: small intestine
R;LaVallie, E.R.; Rehemtulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;
J. Biol. Chem. 268, 23311-23317, 1993
A;Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of b
A;Reference number: A48874; MUID:94043122; PMID:8226855
A;Accession: A48874
A;Molecule type: mRNA
A;Residues: 801-1035 <LAV>
A;Cross-references: GB:L19663; NID:g416131; PIDN:AAA16035.1; PID:g416132
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Light, A.; Janska, H.
J. Protein Chem. 10, 475-480, 1991
A;Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
A;Reference number: A61436; MUID:92189715; PMID:1799406
A;Accession: A61436
A;Molecule type: protein
A;Residues: 801-807,'Y',809-827 <LIG>
C;Comment: The mechanism of association with the membrane of the intestinal brush borde
embrane attachment using a signal-anchor sequence.
C;Comment: Conversion from membrane-bound to soluble forms may involve further processin
C;Complex: mature enteropeptidase is variously reported to contain two (heavy and light)
lfide linked
C;Function:
A;Description: cleaves propeptide from trypsinogen to produce active trypsin
A;Pathway: intestinal digestive hydrolase cascade
C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding rep
C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein
F;22-38/Domain: transmembrane #status predicted <TMM>
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;358-520/Domain: MAM homology <MAM>
F;542-647/Domain: C1r/C1s repeat homology <C1R>
F;659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC
F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>
F;801-1030/Domain: trypsin homology <TRY>
F;116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Bindin
F;788-912,826-842,926-993,957-972,983-1011/Disulfide bonds: #status predicted
F;841,892,987/Active site: His, Asp, Ser #status predicted

  Query Match             27.4%;  Score 669.5;  DB 1;  Length 1035;
  Best Local Similarity   37.0%;  Pred. No. 1.2e-45;
  Matches  146;  Conservative   70;  Mismatches  146;  Indels   33;  Gaps   14;

Qy         66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
              ||||   |    ::|:   :|| |:  |||   |||| ||  |||:       : ::|
Db        652 GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 710

Qy        121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
                : |   |:::|    ::  |  ||  :   : ::   |  |      :|:::

Db        711 IQSIWHVACAENWTTQISDDVCQLLGLGT--GNSSVPTFSTGG---GPYVNLN------- 758

Qy        181 VTALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQAS 233
               || : |: :   : |    ::|||   :|| :   :  | :||||: |    ||| :
Db        759 -TAPNGSLILTPSQQCLEDSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVA 817

Qy        234 LQFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEK 289
               | |    :|| |:::  |:::||||||   : |  |    :||   | | :|   : |:::
Db        818 LYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQ 877

Qy        290 IVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG 349
               || :  |  :|  ||||:| |   : : : |||:|||   : || |::|  :||||
Db        878 IVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQ 937

Qy        350 GDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQE 408
               | : ||  | |||:||: |  :   |   |: :|:|||| ||||||||||||||:|||
Db        938 GSTADVLQEADVPLLSNEKCQQQMPEYN--ITENMVCAGYEAGGVDSCQGDSGGPLMCQE 995

Qy        409 RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
               | | |||| ||  |:|||| ||  | :||
Db        996 NNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWI 1030


RESULT 3
A56318
enteropeptidase (EC 3.4.21.9) precursor [validated] - human
N;Alternate names: enterokinase
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
C;Accession: A56318; B43090
R;Kitamoto, Y.; Veile, R.A.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A;Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolyti
A;Reference number: A56318; MUID:95234679; PMID:7718557
A;Accession: A56318
A;Molecule type: mRNA
A;Residues: 1-1019 <KIT>
A;Cross-references: GB:U09860; NID:g746412; PIDN:AAC50138.1; PID:g746413
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compos
A;Reference number: A43090; MUID:94329561; PMID:8052624
A;Accession: B43090
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 749-1019 <KI2>
A;Cross-references: GB:U09860
C;Comment: The mechanism of association with the membrane of the intestinal brush border
otated below) or with amino-terminal myristoylation of the heavy chain.
C;Genetics:
A;Gene: GDB:PRSS7
A;Cross-references: GDB:384083; OMIM:226200
A;Map position: 21q21-21q21
C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involve
ducts.
C;Function:
A;Description: cleaves activation peptide from trypsinogen to produce active trypsin
A;Pathway: intestinal digestive hydrolase cascade
C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repe
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F;1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
F;22-38/Domain: transmembrane #status predicted <TMM>
F;184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;342-504/Domain: MAM homology <MAM>
F;526-631/Domain: C1r/C1s repeat homology <C1R>
F;643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRCF
F;785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F;785-1014/Domain: trypsin homology <TRY>
F;116,147,179,328,335,388,440,470,503,534,630,682,706,725,848,887,909,949/Binding site: C
F;772-896,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted
F;825,876,971/Active site: His, Asp, Ser #status predicted
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Query Match 27.2%; Score 664.5; DB 1; Length 1019;
Best Local Similarity 37.5%; Pred. No. 2.9e-45;
Matches 147; Conservative 67; Mismatches 149; Indels 29; Gaps 14;

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Qy        67 LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
             |||    |  :  ::|::  :|: |:   |||    |:|| ||  |||          | :::
Db       637 LGIPEPCKADHFQCKNG-ECVPLVNLCDGHLHCEDGSDEADCVRFFNGTTNNNGLVRFRI 695

Qy       122 AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
             : | | |:::|    :|  |  ||  |  ||    : | :|     || : :  ||
Db       696 QSIWHTACAENWTTQISNDVCQLLGLGSGNSSK--PIFSTDG---GPFVKL-NTAPDG-- 747

Qy       182 TALHHSVYVREGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQASLQF 236
                 :   : |    :: |||   :|| :   :  : :||||: :    |||   | :
Db       748 ---HLILTPSQQCLQDSLIRLQCNHKSCGKKLAAQDITPKIVGGSNAKEGAWPWVVGLYY 804

Qy       237 QGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEKIVY 292
               |  ||| |:::  |:::||||||    | |  ||  :||   | | :|     |:::||
Db       805 GGRLLCGASLVSSDWLVSAAHCVYGRNLEPSKWTAILGLHMKSNLTSPQTVPRLIDEIVI 864

Qy       293 HSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDA 352
             :  |  :|  ||||:| |   : : : |||:|||   : || |: |  :|||      |
Db       865 NPHYNRRRKDNDIAMMHLEFKVNYTDYIQPICLPEENQVFPPGRNCSIAGWGTVVYQGTT 924

Qy       353 SPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRL 411
             : :|  | |||:||: |  :   |  |: :|:|||| ||:||||||||||:|||
Db       925 ANILQEADVPLLSNERCQQQMPEYN--ITENMICAGYEEGGIDSCQGDSGGPLMCQENNR 982

Qy       412 WKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
             | | | ||||  ||  |:|||| ||: | :||
Db       983 WFLAGVTSFGYKCALPNRPGVYARVSRFTEWI 1014
```

RESULT 4
A53663
enteropeptidase (EC 3.4.21.9) precursor [validated] - pig
N;Alternate names: enterokinase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
C;Accession: A53663
R;Matsushima, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa,
J. Biol. Chem. 269, 19976-19982, 1994
A;Title: Structural characterization of porcine enteropeptidase.
A;Reference number: A53663; MUID:94327548; PMID:8051081
A;Accession: A53663
A;Molecule type: mRNA
A;Residues: 1-1034 <MAT>
A;Cross-references: GB:D30799; NID:g505122; PIDN:BAA06459.1; PID:g505123
A;Note: parts of this sequence, including the amino ends of three chains isolated from t
C;Comment: The mechanism of association with the membrane of the intestinal brush border
otated below) or with amino-terminal myristoylation of the heavy chain.
C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv
C;Function:
A;Description: cleaves activation peptide from trypsinogen to produce active trypsin
A;Pathway: intestinal digestive hydrolase cascade
C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding rep
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F;22-38/Domain: transmembrane #status predicted <TMM>
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-799/Product: enteropeptidase heavy chain #status predicted <HCH>
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;357-519/Domain: MAM homology <MAM>
F;541-646/Domain: C1r/C1s repeat homology <C1R>
F;658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;693-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC
F;800-1034/Product: enteropeptidase light chain #status predicted <LCH>
F;800-1029/Domain: trypsin homology <TRY>
F;116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902,96
F;787-911,825-841,925-992,956-971,982-1010/Disulfide bonds: #status predicted
F;840,891,986/Active site: His, Asp, Ser #status predicted

Query Match 27.2%; Score 663.5; DB 1; Length 1034;
Best Local Similarity 37.8%; Pred. No. 3.5e-45;
Matches 149; Conservative 65; Mismatches 147; Indels 33; Gaps 14;

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Qy        67 LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
             |||    |    ::| :  :|: |:  ||| | |||| ||  |||          : ::|
Db       652 LGIPEPCKEDNFQCENG-ECVLLVNLCDGFSHCKDGSDEAHCVRFLNGTANNSGLVQFRI 710

Qy       122 AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
             : | | |:::|    ::  |  ||  :  ||      || |      || ::
Db       711 QSIWHTACAENWTTQTSDDVCQLLGLGTGNSSMPF-FSSGGG----PFVKLN-------- 757

Qy       182 TALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQASL 234
             || : |: :   | |    :: |||   :|| :   :  | :|||| |    ||| :|
Db       758 TAPNGSLILTASEQCFEDSLILLQCNHKSCGKKQVAQEVSPKIVGGNDSREGAWPWVVAL 817

Qy       235 QFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEKI 290
             : |  ||| |:::  |:::||||||    | |  |  :||   | | :|    : |:::|
Db       818 YYNGQLLCGASLVSRDWLVSAAHCVYGRNLEPSKWKAILGLHMTSNLTSPQIVTRLIDEI 877

Qy       291 VYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGG 350
             | :  |  :|  :|||:| |   : : : |||:|||   : || |::|  :|||      |
Db       878 VINPHYNRRRKDSDIAMMHLEFKVNYTDYIQPICLPEENQVFPPGRICSIAGWGKVIYQG 937

Qy       351 DASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQER 409
               : :|  | |||:||: |  :   |   |: :|:|||| ||:|||||||||:| |
Db       938 SPADILQEADVPLLSNEKCQQQMPEYN--ITENMMCAGYEEGGIDSCQGDSGGPLMCLEN 995

Qy       410 RLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443
               | | | ||||  ||  |:|||| ||  | :||
Db       996 NRWLLAGVTSFGYQCALPNRPGVYARVPKFTEWI 1029
```

RESULT 5
S33777
hepsin (EC 3.4.21.-) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: S33777; S32013
R;Farley, D.; Reymond, F.; Nick, H.
Biochim. Biophys. Acta 1173, 350-352, 1993
A;Title: Cloning and sequence analysis of rat hepsin, a cell surface serine proteinase.
A;Reference number: S33777; MUID:93305733; PMID:8318546
A;Accession: S33777
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <FAR>
A;Cross-references: EMBL:X70900; NID:g57928; PIDN:CAA50256.1; PID:g57929
C;Superfamily: hepsin; trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;22-44/Domain: transmembrane #status predicted <TMN>
F;162-399/Domain: trypsin homology <TRY>
F;187-203,290-358,321-337,348-380/Disulfide bonds: #status predicted
F;202,256,352/Active site: His, Asp, Ser #status predicted

Query Match 26.8%; Score 654.5; DB 1; Length 416;
Best Local Similarity 35.3%; Pred. No. 6.4e-45;
Matches 146; Conservative 61; Mismatches 156; Indels 51; Gaps 10;

```
Qy        60 ILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQV 119
             : || :|  :     |     :|:  : :: |       | |  |:     | : :| :
Db        17 VAALTVGTLLFLTGIG----AASWAIVTILLR-------SDQEPLYQVQLSPGDSRLLVL 65

Qy       120 -FTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSID----- 173
              |  :|: :||       | : | ::||   ::   | | :          |  :|
Db        66 DKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAHSELDVRTAGANGTSGFFCVDEGGLP 125

Qy       174 ---HLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPW 230
                 ||  | ::          |  |  :|  |  || |:     |||||  | | :|||
Db       126 LAQRLL--DVISVC--------DCPRGRFLTATCQDCGRRKLPVDRIVGGQDSSLGRWPW 175

Qy       231 QASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK------SWTIQVGLVSLLDNPAPS 284
             | ||:: | |||||:::  |::|||||       |:       | :  | |:      |
```

```
Db        176 QVSLRYDGTHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRVFAGAVARTSPHAVQ 230

Qy        285 HLVEKIVYHSKYKPKR------LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVC 338

Db        231 LGVQAVIYHGGYLPFRDPTIDENSNDIALVHLSSSLPLTEYIQPVCLPAAGQALVDGKVC 290

Qy        339 WTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG 398

Db        291 TVTGWGNTQFYGQQAVVLQEARVPIISNEVCNSPDFYGNQIKPKMFCAGYPEGGIDACQG 350

Qy        399 DSGGPLVCQER----RLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448

Db        351 DSGGHFVCEDRISGTSRWRLCGIVSWGTGCALARKPGVYTKVIDFREWIFQAIK 404


RESULT 6
KQRTPL
plasma kallikrein (EC 3.4.21.34) precursor - rat
N;Alternate names: Fletcher factor; kininogenin; serum kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A39180; A33320; S06851; I53041; S06852
R;Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.; Seidah, N.G
Biochemistry 30, 1628-1635, 1991
A;Title: Gene structure and chromosomal localization of plasma kallikrein.
A;Reference number: A39180; MUID:91129236; PMID:1993180
A;Accession: A39180
A;Molecule type: DNA
A;Residues: 1-638 <BEA>
A;Cross-references: GB:J05315
A;Note: the authors translated the codon GAG for residue 81 as Gln
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, F.; Lazur
DNA 8, 563-574, 1989
A;Title: The cDNA structure of rat plasma kallikrein.
A;Reference number: A33320; MUID:90091743; PMID:2598771
A;Accession: A33320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-638 <SEI>
A;Cross-references: GB:M30282; NID:g205010; PIDN:AAA41463.1; PID:g205011
A;Note: part of this sequence, including the amino ends of both the heavy and light chai
R;Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, N.G.
Biochim. Biophys. Acta 999, 103-110, 1989
A;Title: Rat plasma kallikrein: purification, NH(2)-terminal sequencing and development
A;Reference number: S06851; MUID:90089457; PMID:2597701
A;Accession: S06851
A;Molecule type: protein
A;Residues: 20-45;391-413 <PAQ>
R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, R.; Lazur
DNA Cell Biol. 8, 563-574, 1989
A;Title: The cDNA structure of rat plasma kallikrein.
A;Reference number: I53041
A;Accession: I53041
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-638 <RES>
A;Cross-references: GB:M58590; NID:g206721; PIDN:AAA42069.1; PID:g206722
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a li
 are linked by one or more disulfide bonds.
C;Genetics:
A;Gene: PK
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <MAT1>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <MAT2>
F;391-621/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;127,215,308,453,459,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;396/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;434,483,578/Active site: His, Asp, Ser #status predicted

  Query Match           23.7%;  Score 579.5;  DB 1;  Length 638;
  Best Local Similarity  41.0%;  Pred. No. 1.1e-38;
  Matches  116;  Conservative   52;  Mismatches   88;  Indels   27;  Gaps    8;

Qy        189 YVREGCASGHVVTL-------QCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQ---G 238

Db        362 YEAQG-SSGYSLRLCKVVESSDCTT-----KINARIVGGTNSSLGEWPWQVSLQVKLVSQ 415

Qy        239 YHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSL--LDNPAPSHLVEKIVYHSKY 296

Db        416 NHMCGGSIIGRQWILTAAHCFDGIPYPDVWRIYGGILNLSEITNKTPFSSIKELIIHQKY 475

Qy        297 KPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVL 356

Db        476 KMSEGSYDIALIKLQTPLNYTEFQKPICLPSKADTNTIYTNCWVTGWGYTKERGETQNIL 535

Qy        357 NHAAVPLISNKIC--NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKL 414

Db        536 QKATIPLVPNEECQKKYRDY---VITKQMICAGYKEGGIDACKGDSGGPLVCKHSGRWQL 592

Qy        415 VGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM----ERDLKT 453

Db        593 VGITSWGEGCARKEQPGVYTKVAEYIDWILEKIQSSKERALET 635


RESULT 7
KQMSPL
plasma kallikrein (EC 3.4.21.34) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A36557
R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont
DNA Cell Biol. 9, 737-748, 1990
A;Title: Mouse plasma kallikrein: cDNA structure, enzyme characterization, and comparisor
A;Reference number: A36557; MUID:91090844; PMID:2264928
A;Accession: A36557
A;Molecule type: mRNA
A;Residues: 1-638 <SEI>
A;Cross-references: GB:M58588; NID:g200358; PIDN:AAA63393.1; PID:g200359
A;Note: part of this sequence, including the amino ends of both the heavy and light chair
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex wi
C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a lig
 are linked by one or more disulfide bonds.
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflan
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <HCH>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted

  Query Match           23.4%;  Score 570.5;  DB 1;  Length 638;
  Best Local Similarity  34.9%;  Pred. No. 6e-38;
  Matches  126;  Conservative   61;  Mismatches  109;  Indels   65;  Gaps   11;

Qy        132 DWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVR 191

Db        301 DFEGEELNV--------TFVQGADVCQETCTKTIRCQFF-IYSLLPQD---------CKE 342

Qy        192 EGC--------------------ASGHVVTL-------QCTACGHRRGYSSRIVGGNMS 223

Db        343 EGCKCSLRLSTDGSPTRITYGMQGSSGYSLRLCKLVDSPDCTT-----KINARIVGGTNA 397
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Qy        224 LLSQWPWQASLQFQ---GYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSL--L 278
Db        398 SLGEWPWQVSLQVKLVSQTHLCGGSIIGRQWVLTAAHCFDGIPYPDVWRIYGGILSLSEI 457

Qy        279 DNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVC 338
Db        458 TKETPSSRIKELIIHQEYKVSEGNYDIALIKLQTPLNYTEFQKPICLPSKADTNTIYTNC 517

Qy        339 WTSGWGATEDGGDASPVLNHAAVPLISNKIC--NHRDVYGGIISPSMLCAGYLTGGVDSC 396
Db        518 WVTGWGYTKEQGETQNILQKATIPLVPNEECQKKYRDY---VINKQMICAGYKEGGTDAC 574

Qy        397 QGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME----RDLK 452
Db        575 KGDSGGPLVCKHSGRWQLVGITSWGEGCGRKDQPGVYTKVSEYMDWILEKTQSSDVRALE 634

Qy        453 T 453
Db        635 T 635
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RESULT 8
JC7731
membrane-bound arginine-specific serine proteinase precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 03-Feb-2003
C;Accession: JC7731; JC7775
R;Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda,
J. Biochem. 130, 425-430, 2001
A;Title: Characterization of a membrane-bound arginine-specific serine protease from rat
A;Reference number: JC7731; MUID:21421307; PMID:11530019
A;Accession: JC7731
A;Molecule type: mRNA
A;Residues: 1-855 <KIS>
A;Cross-references: DDBJ:AB049189
A;Experimental source: strain Male, 7-week-old
R;Satomi, S.; Yamasaki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001
A;Title: A role for membrane-type serine protease (MT-SP1) in intestinal epithelial turn
A;Reference number: JC7775; PMID:11573963
A;Contents: Small intestine
A;Accession: JC7775
A;Molecule type: mRNA
A;Residues: 1-855 <SAT>
A;Cross-references: DDBJ:AB037898
C;Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease
 of specific proteins or peptides on the brushborder membranes. It also participates in
lial migration and/or cell loss.
C;Genetics:
A;Gene: mt-sp1
A;Map position: basolateral cell surface
C;Superfamily: membrane-bound arginine-specific serine proteinase
C;Keywords: protein digestion

  Query Match   22.6%; Score 553; DB 2; Length 855;
  Best Local Similarity   31.5%; Pred. No. 2.2e-36;
  Matches 135; Conservative   63; Mismatches 148; Indels   82; Gaps   15;

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Qy         73 CSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWKTMCSDD 132
Db        453 CPGMFMCKTG-RCIRKDLRCDGWADCPDYSDERHC------------RCNATHQFMCKNQ 499

Qy        133 ------WKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPD-------- 178
Db        500 FCKPLFWVCDSVN-DCGD-------GSDEEGCSCPAGSFK---CSNGKCLPQSQQCNGKD 548

Qy        179 -----------DKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS------------- 214
Db        549 DCGDGSDEASCDNVNAVSCTKYTYR-CQNGLCLNKGNPECDGKKDCSDGSDEKNCDCGLR 607

Qy        215 -----SRIVGGNMSLLSQWPWQASLQFQGY-HLCGGSVITPLWIITAAHCVYDLYLPK-- 266
Db        608 SFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQDETIFKYS 667

Qy        267 ---SWTIQVGLVSLLDNPA---PSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMI 320
Db        668 DHTMWTAFLGLLDQSKRSASGVQEHKLKRIITHPSFNDFTFDYDIALLELEKPAEYSTVV 727

Qy        321 QPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRDVYGGIIS 380
Db        728 RPICLPDNTHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTC--EELLPQQIT 785

Qy        381 PSMLCAGYLTGGVDSCQGDSGGPLVCQER--RLWKLVGATSFGIGCAEVNKPGVYTRVTS 438
Db        786 PRMMCVGFLSGGVDSCQGDSGGPLSSVEKDGRIFQ-AGVVSWGEGCAQRNKPGVYTRIPE 844

Qy        439 FLDWIHEQ 446
Db        845 VRDWIKEQ 852
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RESULT 9
KQHUP
plasma kallikrein (EC 3.4.21.34) precursor - human
N;Alternate names: kininogenin; plasma prekallikrein
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: A00921; A37939
R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four t
A;Reference number: A00921; MUID:86243359; PMID:3521732
A;Accession: A00921
A;Molecule type: mRNA
A;Residues: 1-638 <CHU>
A;Cross-references: GB:M13143; NID:g190262; PIDN:AAA60153.1; PID:g190263
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
A;Reference number: A37939; MUID:91152016; PMID:1998666
A;Accession: A37939
A;Molecule type: protein
A;Residues: 20-27;40-46,'X',48,'H';50,'X',52-70,'H';75-76,'X',78-80;103-113;131-140;141-
;260-283,'X',285;287-291,'X',293-295;314-317,'X',319-320;321-324;'X',329-333;334-339,'X'
525;538-551;562,'X',564-567;573,'X',575-576;578-583,'X',585;592-604 <MCM>
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a li
 are linked by one or more disulfide bonds.
C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal r
inogen and may also play a role in the renin-angiotensin system by converting prorenin i
C;Genetics:
A;Gene: GDB:KLK3
A;Cross-references: GDB:127575; OMIM:229000
A;Map position: 4q35-4q35
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflam
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-638/Product: plasma kallikrein #status predicted <MAT>
F;20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
F;127,308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;318-347,340-345/Disulfide bonds: #status predicted
F;390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted

  Query Match   22.5%; Score 549.5; DB 1; Length 638;
  Best Local Similarity   35.8%; Pred. No. 2.9e-36;
  Matches 124; Conservative   57; Mismatches 116; Indels   49; Gaps   11;

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Qy        132 DWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDD------------ 179
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Db        301 DFGGEELNV--------TFVKGVNVCQETCTKMIRCQFFTYS-LLPEDCKEEKCKCFLRL 351

Qy        180 ----KVTALHHSVYVREGCASGHVVTL-------QCTACGHRRGYSSRIVGGNMSLLSQW 228

Db        352 SMDGSPTRI---AYGTQG-SSGYSLRLCNTGDNSVCTT-----KTSTRIVGGTNSSWGEW 402

Qy        229 PWQASLQFQ---GYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLD--NPAP 283

Db        403 PWQVSLQVKLTAQRHLCGGSLIGHQWVLTAAHCFDGLPLQDVWRIYSGILNLSDITKDTP 462

Qy        284 SHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGW 343

Db        463 FSQIKEIIIHQNYKVSEGNHDIALIKLQAPLNYTEFQKPICLPSKGDTSTIYTNCWVTGW 522

Qy        344 GATEDGGDASPVLNHAAVPLISNKICNHRDVYGGI-ISPSMLCAGYLTGGVDSCQGDSGG 402

Db        523 GFSKEKGEIQNILQKVNIPLVTNEECQKR--YQDYKITQRMVCAGYKEGGKDACKGDSGG 580

Qy        403 PLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 448

Db        581 PLVCKHNGMWRLVGITSWGEGCARREQPGVYTKVAEYMDWILEKTQ 626


RESULT 10
JC5759
brain-specific serine proteinase (EC 3.4.21.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 31-Mar-2000
C;Accession: JC5759
R;Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.; Tsujimura, A.; Yamaguchi, N.
Biochem. Biophys. Res. Commun. 239, 386-392, 1997
A;Title: Molecular cloning of a novel brain-specific serine protease with a kringle-like
A;Reference number: JC5759; MUID:98008848; PMID:9344839
A;Accession: JC5759
A;Molecule type: mRNA
A;Residues: 1-761 <YAM>
A;Cross-references: DDBJ:D89871
A;Experimental source: brain
C;Superfamily: brain-specific serine proteinase; scavenger receptor cysteine-rich domain
C;Keywords: glycoprotein; hydrolase; serine proteinase
F;85-157/Domain: kringle-like #status predicted <KRI>
F;163-266/Domain: scavenger receptor cysteine-rich domain homology <SRC7>
F;166-266,273-372,386-486/Domain: scavenger receptor cysteine-rich #status predicted <SR
F;513-516/Domain: furin binding #status predicted <FRB>
F;517-755/Domain: trypsin homology <TRY>
F;93,521,569/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;562,612,711/Active site: His, Asp, Ser #status predicted

  Query Match             21.6%;  Score 527;  DB 2;  Length 761;
  Best Local Similarity   31.9%;  Pred. No. 2.3e-34;
  Matches  147;  Conservative   53;  Mismatches  143;  Indels  118;  Gaps   21;

Qy         70 HFD------------CSGKYRCRSSFKCIELIARCDGVSDCKDGED-------------- 103

Db        326 HFDGSNRPIWLDDVSCSGK---EVSF--IQCSRRQWGRHDCSHREDVGLTCYPDSDGHRL 380

Qy        104 --EYRCVRVGGQN---AVLQVFTAASWKTMCSDDWKGHYANVACAQLGFP--------SY 150

Db        381 SPGFPIRLVDGENKKEGRVEVFVNGQWGTICDDGWTDKHAAVICRQLGYKGPARARTMAY 440

Qy        151 -------VSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSV-------YVREGCAS 196

Db        441 PGEGKGPIHMDNVKCTG------NEKALADCVKQDIGRHNCRHSEDAGVICDYLEKKASS 494

Qy        197 GHVVTLQCTACG----HRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH-----LCGGSVI 247

Db        495 SGNKEMLSSGCGLRLLHRR--QKRIIGGNNSLRGAWPWQASLRLRSAHGDGRLLCGATLL 552

Qy        248 TPLWIITAAHCV----------------YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV 291

Db        553 SSCWVLTAAHCFKRYGNNSRSYAVRVGDYHTLVPEEFEQEIG-------------VQQIV 599

Qy        292 YHSKYKPKRLGNDIALMKLAGP----LTFNEMIQPVCLPNSEENFPD--GKVCWTSGWGA 345

Db        600 IHRNYRPDRSDYDIALVRLQGPGEQCARLSTHVLPACLPLWRER-PQKTASNCHITGWGD 658

Qy        346 TEDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYL--TGGVDSCQGDSGGP 403

Db        659 T--GRAYSRTLQQAAVPLLPKRFCKER--YKGLFTGRMLCAGNLQEDNRVDSCQGDSGGP 714

Qy        404 LVCQE-RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 443

Db        715 LMCEKPDESWVVYGVTSWGYGCGVKDTPGVYTRVPAFVPWI 755


RESULT 11
A61545
plasmin (EC 3.4.21.7) precursor - horse (fragments)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: A61545; S17527
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69,_1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: A61545
A;Molecule type: protein
A;Residues: 1-33;34-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A;Title: Complete amino acid sequence of equine miniplasminogen.
A;Reference number: S17527; MUID:92052077; PMID:1946332
A;Accession: S17527
A;Molecule type: protein
A;Residues: 118-455 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
F;1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
F;1-33/Domain: activation peptide (fragment) #status experimental <APT>
F;34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
F;37-114/Domain: kringle homology <KR4>
F;118-455/Product: miniplasminogen #status experimental <MIN>
F;126-205/Domain: kringle homology <KR5>
F;226-455/Domain: plasmin chain B #status experimental <BCH>
F;226-448/Domain: trypsin homology <TRY>
F;267,310,405/Active site: His, Asp, Ser #status predicted

  Query Match             21.5%;  Score 526;  DB 2;  Length 455;
  Best Local Similarity   42.0%;  Pred. No. 1.5e-34;
  Matches  107;  Conservative   47;  Mismatches   87;  Indels   14;  Gaps    6;

Qy        203 QCTA----CG----HRRGYSSRIVGGNMSLLSQWPWQASLQFQ-GYHLCGGSVITPLWII 253

Db        204 QCESSPFDCGKPKVEPKKCSGRIVGGCVAIAHSWPWQISLRTRFGRHFCGGTLISPEWVL 263

Qy        254 TAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGP 313

Db        264 TAAHCLERSSRPSTYKVVLGTHHELRLAAGAQQID--VSKLFLEPSRA--DIALLKLSSP 319

Qy        314 LTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHRD 373

Db        320 AIITQNVIPACLPPADYVVANWAECFVTGWGETQDSSNAG-VLKEAQLPVIENKVCNRYE 378

Qy        374 VYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVY 433

Db        379 YLNGRVKSTELCAGHLVGGVDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVY 438

Qy        434 TRVTSFLDWIHEQME 448

Db        439 VRVSSFINWIERIMQ 453


RESULT 12
```

```
PLPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A;Reference number: S03733
A;Accession: S03733
A;Molecule type: protein
A;Residues: 1-560 <SCH>
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03737
A;Molecule type: protein
A;Residues: 1-57 <BRU>
R;Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A;Reference number: A25834; MUID:85203907; PMID:3846533
A;Accession: A25834
A;Molecule type: protein
A;Residues: 450-790 <MAR>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F;1-790/Product: plasminogen #status predicted <PRO>
F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F;1-77/Domain: activation peptide #status predicted <APT>
F;78-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B #status experimental <BCH>
F;561-783/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
bonds: #status predicted
F;602,645,740/Active site: His, Asp, Ser #status predicted

  Query Match             21.4%;  Score 523.5;  DB 1;  Length 790;
  Best Local Similarity   41.4%;  Pred. No. 4.6e-34;
  Matches  108;  Conservative   43;  Mismatches   89;  Indels   21;  Gaps    6;

Qy        194 CASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGY--HLCGGSVITPLW 251
              |      |    :| |          |:||| :|:   |||| ||::: |  | |||::|:| |
Db        547 CGKPKVEPKKCPA---------RVVGGCVSIPHSWPWQISLRYR-YRGHFCGGTLISPEW 596

Qy        252 IITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKI--VYHSKYKPKRLGNDIALMK 309
              ::|| ||:      | |: :      :|      || | :  :  ||    :    ||||:|
Db        597 VLTAKHCLEKSSSPSSYKV------ILGAHEEYHLGEGVQEIDVSKLFKEPSEADIALLK 650

Qy        310 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKIC 369
              |: |     : : | |||          |    |: :||| |: |    : :|   | :|:| ||:|
Db        651 LSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETK-GTYGAGLLKEARLPVIENKVC 709

Qy        370 NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNK 429
              |  :   || :||: ||||:| ||:|||||||||||||| |:  :  | | ||:|:|||   ||
Db        710 NRYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCALPNK 769

Qy        430 PGVYTRVTSFLDWIHEQMERD 450
              |||| ||: |: || | | |:
Db        770 PGVYVRVSRFVTWIEEIMRRN 790
```

```
RESULT 13
JE0315
low-density lipoprotein receptor-related protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Feb-2003
C;Accession: JE0315
R;Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.
J. Biochem. 124, 784-789, 1998
A;Title: A novel low-density lipoprotein receptor-related protein with type II membrane p
A;Reference number: JE0315; MUID:98429596; PMID:9756624
A;Accession: JE0315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1113 <TOM>
A;Cross-references: DDBJ:AB013874; NID:g3869144; PIDN:BAA34371.1; PID:g3869145
C;Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor ligar
F;337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;648-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;869-1097/Domain: trypsin homology <TRY>

  Query Match             20.7%;  Score 506.5;  DB 2;  Length 1113;
  Best Local Similarity   31.7%;  Pred. No. 1.6e-32;
  Matches  126;  Conservative   76;  Mismatches  160;  Indels   35;  Gaps   16;

Qy         72 DCS----GKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV---GGQNAVLQVFTAAS 124
              :||     :  | :: :|:     |||  || |  ||: || :    |  :::| |  :|
Db        719 NCSFCQDNELEC-ANHECVPRDLWCDGWVDCSDSSDEWGCVTLSKNGNSSSLLTVHKSAK 777

Qy        125 WKTMCSDDWKGHYANVACAQLGF--PSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVT 182
                :|:| |:   : :|| |:|   ||          : ||  :::: :     :   :
Db        778 EHHVCADGWRETLSQLACKQMGLGEPSV-------TKLIPGQEGQQWLRLYPNWENLNGS 830

Qy        183 ALHHSVYVREGCASGHVVTLQCTA--CGHRRG--YSSRIVGGNMSLLSQWPWQASLQFQ- 237
              |   :  |  | |   ::| |:   || |     : ||:||  |   :|||| ||| :
Db        831 TLQELLVYRHSCPSRSEISLLCSKQDCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSEP 890

Qy        238 GYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPA---PSHLVEKIVYHS 294
              |:||  :|   |::| |||          | :  | :: ||:|:    :  |: |: |
Db        891 SGHICGCVLIAKKWVLTVAHCFEGREDADVWKVVFG-INNLDHPSGFMQTRFVKTILLHP 949

Qy        295 KYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASP 354
              :|    :  ||:::|:  :     ::|||||: ||        |: :|||     |:  |
Db        950 RYSRAVVDYDISVVELSDDINETSYVRPVCLPSPEEYLEPDTYCYITGWGHM---GNKMP 1006

Qy        355 V-LNHAAVPLISNKIC-NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQE-RRL 411
              |     | :|  : | ::  |:     |:  |:|||| :| |||| |||||||||:
Db       1007 FKLQEGEVRIIPLEQCQSYFDM--KTITNRMICAGYESGTVDSCMGDSGGPLVCERPGGQ 1064

Qy        412 WKLVGATSFGIGC-AEVNKPGVYTRVTSFLDWIHEQM 447
              | | | ||:|  | ::|  ||||: |: |: ||  |:
Db       1065 WTLFGLTSWGSVCFSKVLGPGVYSNVSYFVGWIERQI 1101


RESULT 14
A47246
tryptase (EC 3.4.21.59) 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47246
R;McNeil, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.; S
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast c
A;Reference number: A47246; MUID:93087489; PMID:1454796
A;Accession: A47246
A;Status: preliminary
A;Molecule type: nucleic acid
```

```
A;Residues: 1-273 <MCN>
A;Cross-references: GB:L00653; NID:g200518; PIDN:AAA39992.1; PID:g200519
A;Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBIP:119746)
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;29-265/Domain: trypsin homology <TRY>

  Query Match             20.6%;  Score 504;  DB 2;  Length 273;
  Best Local Similarity   42.2%;  Pred. No. 5e-33;
  Matches  105;  Conservative   40;  Mismatches   84;  Indels   20;  Gaps    8;

Qy        217 IVGGNMSLLSQWPWQASLQFQG---YHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQV 272
              ||||   :  ::|||| ||:       | ||||:| | |::|||||  |:  |    :|:
Db         29 IVGGQEAHGNKWPWQVSLRANDTYWMHFCGGSLIHPQWVLTAAHCVGPDVADPNKVRVQL 88

Qy        273 GLVSLLDNPAPSHL--VEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEE 330
                 |  :    ||  | :|: |   :   : | ||||:||  |:  :: : || || : |
Db         89 RKQYLYYH---DHLMTVSQIITHPDFYIVQDGADIALLKLTNPVNISDYVHPVPLPPASE 145

Qy        331 NFPDGKVCWTSGWGATEDGGDASP--VLNHAAVPLISNKICN---HRDVYGG----IISP 381
              || | :|| :|||  ::| :  |   |    ||:| | :|:   |: :  |    |:
Db        146 TFPSGTLCWVTGWGNIDNGVNLPPPFPLKEVQVPIIENHLCDLKYHKGLITGDNVHIVRD 205

Qy        382 SMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLD 441
              |||||    | ||||||||||||||:    |   |  |:| |||: |:|:|||||| :||
Db        206 DMLCAG--NEGHDSCQGDSGGPLVCKVEDTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLD 263

Qy        442 WIHEQMERD 450
              |||  : :|
Db        264 WIHHYVPKD 272


RESULT 15
KFHU1
coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human
N;Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-Dec-2000
C;Accession: A27431; A00920; A37940
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Biochemistry 26, 7221-7228, 1987
A;Title: Organization of the gene for human factor XI.
A;Reference number: A27431; MUID:88107663; PMID:2827746
A;Accession: A27431
A;Molecule type: DNA
A;Residues: 1-625 <ASA>
A;Cross-references: GB:M18295
A;Note: the sequence shown follows the authors' translation
R;Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
A;Title: Amino acid sequence of human factor XI, a blood coagulation factor with four ta
A;Reference number: A00920; MUID:86243360; PMID:3636155
A;Accession: A00920
A;Molecule type: mRNA
A;Residues: 1-625 <FUJ>
A;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2056-2060, 1991
A;Title: Location of the disulfide bonds in human coagulation factor XI: the presence of
A;Reference number: A37940; MUID:91152017; PMID:1998667
A;Accession: A37940
A;Molecule type: protein
A;Residues: 28-33;35-49,'X',51-55,'X',57-63;70-75,'X',77-79;107-109,'X',111-112;132-139;
;280-282,'X',284;285-297;313-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375
C;Comment: The proenzyme consists of two identical chains linked by one or more disulfic
he active site, and a heavy chain, which associates with high molecular weight (HMW) kin
C;Genetics:
A;Gene: GDB:F11
A;Cross-references: GDB:119891; OMIM:264900
A;Map position: 4q35-4q35
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor IX
A;Pathway: blood coagulation intrinsic pathway
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydrol
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-387/Product: coagulation factor XIa heavy chain #status experimental <HCH>
F;19-108/Domain: apple repeat <AP1>
F;109-198/Domain: apple repeat <AP2>
F;199-288/Domain: apple repeat <AP3>
F;290-379/Domain: apple repeat <AP4>
F;388-625/Product: coagulation factor XIa light chain #status experimental <LCH>
F;388-618/Domain: trypsin homology <TRY>
F;20-103,514-581,571-599/Disulfide bonds: #status predicted
F;29/Disulfide bonds: interchain #status experimental
F;46-76,50-56,110-193,136-165,140-146,200-283,226-255,230-236,291-374,317-346,321-327,38(
F;90,126,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;339/Disulfide bonds: interchain #status predicted
F;387-388/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;431,480,575/Active site: His, Asp, Ser #status predicted
F;491/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             20.6%;  Score 504;  DB 1;  Length 625;
  Best Local Similarity   38.7%;  Pred. No. 1.3e-32;
  Matches  103;  Conservative   44;  Mismatches  103;  Indels   16;  Gaps    5;

Qy        193 GCASGHVVTL-----QCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQG---YHLCGG 244
              |  ||: : |     :||          |||||  |:  :|||| :|       |||||
Db        364 GGISGYTLRLCKMDNECTT-----KIKPRIVGGTASVRGEWPWQVTLHTTSPTQRHLCGG 418

Qy        245 SVITPLWIITAAHCVYDLYLPKSWTIQVGLV--SLLDNPAPSHLVEKIVYHSKYKPKRLG 302
              |:|   ||:||||| | :  ||   :  |::  | :         |::|: | :||    |
Db        419 SIIGNQWILTAAHCFYGVESPKILRVYSGILNQSEIKEDTSFFGVQEIIIHDQYKMAESG 478

Qy        303 NDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVP 362
              ||||:||   : : :  :|:|||:  :        || :|||  :         |  | :|
Db        479 YDIALLKLETTVNYTDSQRPICLPSKGDRNVIYTDCWVTGWGYRKLRDKIQNTLQKAKIP 538

Qy        363 LISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGI 422
              |::|: |  |   |  |:  |:|||| || |:|:|||||| |:   :| ||| ||:|
Db        539 LVTNEECQKR-YRGHKITHKMICAGYREGGKDACKGDSGGPLSCKHNEVWHLVGITSWGE 597

Qy        423 GCAEVNKPGVYTRVTSFLDWIHEQME 448
              |||:  :|||| |  ::||| |: :
Db        598 GCAQRERPGVYTNVVEYVDWILEKTQ 623


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Job time : 21 secs
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